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(72) **Inventors;** and
(75) **Inventors/Applicants (for US only):** YUQIU, Jiang [CN/US]; 5001 South 232nd Street, Kent, WA 98032 (US). MITCHAM, Jennifer, L. [US/US]; 16677 NE 88th Street, Redmond, WA 98052 (US).

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(71) **Applicant (for all designated States except US): CORIXA CORPORATION [US/US]**; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).

(74) **Agents:** POTTER, Jane, E., R.; Seed Intellectual Property Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seattle, WA 98104-7092 et al. (US).

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(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF BREAST CANCER

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(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as breast cancer, are disclosed. Compositions may comprise one or more breast tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a breast tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as breast cancer. Diagnostic methods based on detecting a breast tumor protein, or mRNA encoding such a protein, in a sample are also provided.



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COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF BREAST CANCER

TECHNICAL FIELD OF THE INVENTION

The present invention relates generally to therapy and diagnosis of cancer, such as breast cancer. The invention is more specifically related to polypeptides comprising at least a portion of a breast tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for prevention and treatment of breast cancer, and for the diagnosis and monitoring of such cancers.

10 BACKGROUND OF THE INVENTION

Breast cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in detection and treatment of the disease, breast cancer remains the second leading cause of cancer-related deaths in women, affecting more than 180,000 women in the United States each year. For women in North America, the life-time odds of getting breast cancer are now one in eight.

No vaccine or other universally successful method for the prevention or treatment of breast cancer is currently available. Management of the disease currently relies on a combination of early diagnosis (through routine breast screening procedures) and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular breast cancer is often selected based on a variety of prognostic parameters, including an analysis of specific tumor markers. *See, e.g.,* Porter-Jordan and Lippman, *Breast Cancer* 8:73-100, 1994. However, the use of established markers often leads to a result that is difficult to interpret, and the high mortality observed in breast cancer patients indicates that improvements are needed in the treatment, diagnosis and prevention of the disease.

Immunotherapies have the potential to substantially improve breast cancer treatment and survival. Such therapies may involve the generation or

enhancement of an immune response to a breast tumor antigen. However, to date, relatively few breast tumor antigens are known and the generation of an immune response against such antigens has not been shown to be therapeutically beneficial.

Accordingly, there is a need in the art for improved methods for identifying breast tumor antigens and for using such antigens in the diagnosis and therapy of breast cancer. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the diagnosis and therapy of cancer, such as breast cancer. In one aspect, the present invention provides polypeptides comprising at least a portion of a breast tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises a sequence that is encoded by a polynucleotide sequence selected from the group consisting of sequences recited in SEQ ID NOs:1-125, variants of such sequences and complements of such sequences. One such polypeptide comprises a sequence recited in SEQ ID NO:126, or a variant thereof that is at least 90% identical to SEQ ID NO:126.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 9, preferably at least 15, amino acid residues of a breast tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and a non-specific immune response enhancer.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a breast tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages and B cells.

Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a non-specific immune response enhancer.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein or a polynucleotide encoding a fusion protein in combination with a non-specific immune response enhancer.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a breast tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a breast tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such 5 a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a 10 patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a breast tumor protein; (ii) a 15 polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expresses such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

20 Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a 25 predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be breast cancer.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps 30 of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the

sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the 5 patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a breast tumor protein; (b) detecting in the 10 sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one 15 oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

20 In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a breast tumor protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) 25 using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

30 Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as

diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All 5 references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWING

Figure 1 represents a sequence alignment between the representative breast tumor polypeptide B1002C (SEQ ID NO:126) and the mouse iroquois homeobox 10 protein 3.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for using the compositions, for example in the therapy and diagnosis of cancer, such as breast cancer. Certain illustrative compositions described 15 herein include breast tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (e.g., T cells). A "breast tumor protein," as the term is used herein, refers generally to a protein that is expressed in breast tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal 20 tissue, as determined using a representative assay provided herein. Certain breast tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with breast cancer.

Therefore, in accordance with the above, and as described further below, the present invention provides illustrative polynucleotide compositions having 25 sequences set forth in SEQ ID NO:1-125, illustrative polypeptide compositions having amino acid sequences set forth in SEQ ID NO:126, antibody compositions capable of binding such polypeptides, and numerous additional embodiments employing such compositions, for example in the detection, diagnosis and/or therapy of human breast cancer.

POLYNUCLEOTIDE COMPOSITIONS

As used herein, the terms "DNA segment" and "polynucleotide" refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. Therefore, a DNA segment encoding a polypeptide refers to a DNA segment 5 that contains one or more coding sequences yet is substantially isolated away from, or purified free from, total genomic DNA of the species from which the DNA segment is obtained. Included within the terms "DNA segment" and "polynucleotide" are DNA segments and smaller fragments of such segments, and also recombinant vectors, including, for example, plasmids, cosmids, phagemids, phage, viruses, and the like.

10 As will be understood by those skilled in the art, the DNA segments of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may be naturally isolated, or modified synthetically by the hand of man.

15 "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA segment does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA segment as originally isolated, and does not exclude genes or coding regions later added 20 to the segment by the hand of man.

As will be recognized by the skilled artisan, polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and 25 mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous 30 sequence that encodes a breast tumor protein or a portion thereof) or may comprise a variant, or a biological or antigenic functional equivalent of such a sequence.

Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions, as further described below, preferably such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as 5 described herein. The term "variants" also encompasses homologous genes of xenogenic origin.

When comparing polynucleotide or polypeptide sequences, two sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence, as described 10 below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions 15 after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A 20 model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) 25 *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

30 Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL.*

Math 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics 5 Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.* (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be 10 calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the 15 cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix 20 (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by 25 comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the 30 comparison window may comprise additions or deletions (i.e., gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference

sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the 5 total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Therefore, the present invention encompasses polynucleotide and polypeptide sequences having substantial identity to the sequences disclosed herein, for example those comprising at least 50% sequence identity, preferably at least 55%, 60%, 10 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide or polypeptide sequence of this invention using the methods described herein, (*e.g.*, BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two 15 nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

In additional embodiments, the present invention provides isolated polynucleotides and polypeptides comprising various lengths of contiguous stretches of sequence identical to or complementary to one or more of the sequences disclosed 20 herein. For example, polynucleotides are provided by this invention that comprise at least about 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 25 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through 200-500; 500-1,000, and the like.

The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other 30 DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their

overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative DNA segments with total lengths of about 10,000, about 5000, 5 about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

In other embodiments, the present invention is directed to polynucleotides that are capable of hybridizing under moderately stringent conditions to 10 a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM 15 EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

Moreover, it will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences 20 that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. 25 Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

PROBES AND PRIMERS

In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise 5 a sequence region of at least about 15 nucleotide long contiguous sequence that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence disclosed herein will find particular utility. Longer contiguous identical or complementary sequences, *e.g.*, those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) and even up to full length sequences will also be of 10 use in certain embodiments.

The ability of such nucleic acid probes to specifically hybridize to a sequence of interest will enable them to be of use in detecting the presence of complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species 15 primers, or primers for use in preparing other genetic constructions.

Polynucleotide molecules having sequence regions consisting of contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as 20 hybridization probes for use in, *e.g.*, Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in various bacterial cells. The total size of fragment, as well as the size of the complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in 25 hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger contiguous complementarity stretches may be used, according to the length complementary sequences one wishes to detect.

The use of a hybridization probe of about 15-25 nucleotides in length 30 allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in

length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where

5 desired.

Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequence set forth in SEQ ID NO:1-125, or to any continuous portion of the sequence, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to

10 utilize as a probe or primer. The choice of probe and primer sequences may be governed by various factors. For example, one may wish to employ primers from towards the termini of the total sequence.

Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly

15 practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCR™ technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular

20 biology.

The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of

25 selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, *e.g.*, one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate

30 little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one

5 may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to

10 destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

POLYNUCLEOTIDE IDENTIFICATION AND CHARACTERIZATION

Polynucleotides may be identified, prepared and/or manipulated using

15 any of a variety of well established techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least two fold greater in a tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed, for example, using a Synteni microarray (Palo Alto,

20 CA) according to the manufacturer's instructions (and essentially as described by Schena *et al.*, *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller *et al.*, *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as breast tumor cells. Such polynucleotides may be amplified via polymerase

25 chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (*e.g.*, a breast tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or

30 genomic) is screened using one or more polynucleotide probes or primers suitable for

amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

5 For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor 10 Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping 15 clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining 20 a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target 25 sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (see Triglia *et al.*, *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment 30 in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known

region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known 5 region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' 10 and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom *et al.*, *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker *et al.*, *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence 15 by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

20 POLYNUCLEOTIDE EXPRESSION IN HOST CELLS

In other embodiments of the invention, polynucleotide sequences or 25 fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous 30 in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular

prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

5 Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene
10 fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or
15 recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding
20 sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. *et al.* (1980) *Nucl. Acids Res. Symp. Ser.* 215-223, Horn, T. *et al.* (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. *et al.* (1995) *Science* 269:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo
30 Alto, CA).

A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, T. (1983) Proteins, Structures and Molecular Principles, WH Freeman and Co., New York, N.Y.) or other comparable techniques available in the art. The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

10 In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing 15 sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described in Sambrook, J. *et al.* (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. *et al.* (1989) Current 20 Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y.

A variety of expression vector/host systems may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; 25 insect cell systems infected with virus expression vectors (e.g., baculovirus); plant cell systems transformed with virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems.

The "control elements" or "regulatory sequences" present in an 30 expression vector are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular proteins to carry out

transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid 5 lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPORT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are generally preferred. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV 10 may be advantageously used with an appropriate selectable marker.

In bacterial systems, a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example, when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. 15 Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of .beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. 20 Biol. Chem.* 264:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to 25 include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel *et al.* (supra) and Grant *et al.* (1987) *Methods 30 Enzymol.* 153:516-544.

In cases where plant expression vectors are used, the expression of sequences encoding polypeptides may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. 5 (1987) *EMBO J.* 6:307-311. Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. *et al.* (1984) *EMBO J.* 3:1671-1680; Broglie, R. *et al.* (1984) *Science* 224:838-843; and Winter, J. *et al.* (1991) *Results Probl. Cell Differ.* 17:85-105). These constructs can be introduced into plant 10 cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

An insect system may also be used to express a polypeptide of interest. For example, in one such system, *Autographa californica* nuclear polyhedrosis virus 15 (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat 20 protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or *Trichoplusia* larvae in which the polypeptide of interest may be expressed (Engelhard, E. K. *et al.* (1994) *Proc. Natl. Acad. Sci.* 91:3224-3227).

In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression 25 vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci.* 81:3655-3659). In addition, 30 transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the 5 appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational 10 elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. *et al.* (1994) *Results Probl. Cell Differ.* 20:125-162).

In addition, a host cell strain may be chosen for its ability to modulate 15 the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as 20 CHO, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a 25 polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer 30 resistance to selection, and its presence allows growth and recovery of cells which

successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. *et al.* (1977) *Cell* 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. *et al.* (1990) *Cell* 22:817-23) genes which can be employed in tk.sup.- or aprt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. *et al.* (1980) *Proc. Natl. Acad. Sci.* 77:3567-70); npt, which 5 confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. *et al* (1981) *J. Mol. Biol.* 150:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells 10 to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci.* 85:8047-51). Recently, the use of visible markers has gained popularity with such 15 markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific 20 vector system (Rhodes, C. A. *et al.* (1995) *Methods Mol. Biol.* 55:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the 25 absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells which contain and express a desired 30 polynucleotide sequence may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-

RNA hybridizations and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

A variety of protocols for detecting and measuring the expression of 5 polynucleotide-encoded products, using either polyclonal or monoclonal antibodies specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on a given polypeptide may be 10 preferred for some applications, but a competitive binding assay may also be employed. These and other assays are described, among other places, in Hampton, R. *et al.* (1990; Serological Methods, a Laboratory Manual, APS Press, St Paul. Minn.) and Maddox, D. E. *et al.* (1983; *J. Exp. Med.* 158:1211-1216).

A wide variety of labels and conjugation techniques are known by those 15 skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions thereof may be cloned into a vector for the production of an mRNA probe. Such vectors 20 are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents 25 as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood 30 by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of the

encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. *et al.* (1992, *Prot. Exp. Purif.* 3:263-281) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. *et al.* (1993; *DNA Cell Biol.* 12:441-453).

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc.* 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

SITE-SPECIFIC MUTAGENESIS

Site-specific mutagenesis is a technique useful in the preparation of individual peptides, or biologically functional equivalent polypeptides, through specific mutagenesis of the underlying polynucleotides that encode them. The technique,

well-known to those of skill in the art, further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific 5 oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the 10 properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or more properties of the encoded polypeptide, such as the antigenicity of a polypeptide 15 vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25 nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of 20 the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily 25 commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of 30 a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated

sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original 5 non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding 10 DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence 15 variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation 20 which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent 25 process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of 30 the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

POLYNUCLEOTIDE AMPLIFICATION TECHNIQUES

A number of template dependent processes are available to amplify the target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. 5 Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by reference in its entirety. Briefly, in PCR™, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (e.g., *Taq* polymerase). If the target sequence is present 10 in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse 15 transcription and PCR™ amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Another method for amplification is the ligase chain reaction (referred to as LCR), disclosed in Eur. Pat. Appl. Publ. No. 320,308 (specifically incorporated 20 herein by reference in its entirety). In LCR, two complementary probe pairs are prepared, and in the presence of the target sequence, each pair will bind to opposite complementary strands of the target such that they abut. In the presence of a ligase, the two probe pairs will link to form a single unit. By temperature cycling, as in PCR™, bound ligated units dissociate from the target and then serve as "target sequences" for 25 ligation of excess probe pairs. U.S. Patent No. 4,883,750, incorporated herein by reference in its entirety, describes an alternative method of amplification similar to LCR for binding probe pairs to a target sequence.

Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880, incorporated herein by reference in its entirety, may also be used as 30 still another amplification method in the present invention. In this method, a replicative sequence of RNA that has a region complementary to that of a target is added to a

sample in the presence of an RNA polymerase. The polymerase will copy the replicative sequence that can then be detected.

An isothermal amplification method, in which restriction endonucleases and ligases are used to achieve the amplification of target molecules that contain 5 nucleotide 5'-[α -thio]triphosphates in one strand of a restriction site (Walker *et al.*, 1992, incorporated herein by reference in its entirety), may also be useful in the amplification of nucleic acids in the present invention.

Strand Displacement Amplification (SDA) is another method of carrying out isothermal amplification of nucleic acids which involves multiple rounds of strand 10 displacement and synthesis, *i.e.* nick translation. A similar method, called Repair Chain Reaction (RCR) is another method of amplification which may be useful in the present invention and is involves annealing several probes throughout a region targeted for amplification, followed by a repair reaction in which only two of the four bases are present. The other two bases can be added as biotinylated derivatives for easy 15 detection. A similar approach is used in SDA.

Sequences can also be detected using a cyclic probe reaction (CPR). In CPR, a probe having a 3' and 5' sequences of non-target DNA and an internal or "middle" sequence of the target protein specific RNA is hybridized to DNA which is present in a sample. Upon hybridization, the reaction is treated with RNaseH, and the 20 products of the probe are identified as distinctive products by generating a signal that is released after digestion. The original template is annealed to another cycling probe and the reaction is repeated. Thus, CPR involves amplifying a signal generated by hybridization of a probe to a target gene specific expressed nucleic acid.

Still other amplification methods described in Great Britain Pat. Appl. 25 No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025, each of which is incorporated herein by reference in its entirety, may be used in accordance with the present invention. In the former application, "modified" primers are used in a PCR-like, template and enzyme dependent synthesis. The primers may be modified by labeling with a capture moiety (*e.g.*, biotin) and/or a detector moiety (*e.g.*, enzyme). In 30 the latter application, an excess of labeled probes is added to a sample. In the presence of the target sequence, the probe binds and is cleaved catalytically. After cleavage, the

target sequence is released intact to be bound by excess probe. Cleavage of the labeled probe signals the presence of the target sequence.

Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (Kwoh *et al.*, 1989; PCT Int'l. Pat. Appl. Publ. No. WO 5 88/10315, incorporated herein by reference in its entirety), including nucleic acid sequence based amplification (NASBA) and 3SR. In NASBA, the nucleic acids can be prepared for amplification by standard phenol/chloroform extraction, heat denaturation of a sample, treatment with lysis buffer and minispin columns for isolation of DNA and RNA or guanidinium chloride extraction of RNA. These amplification techniques 10 involve annealing a primer that has sequences specific to the target sequence. Following polymerization, DNA/RNA hybrids are digested with RNase H while double stranded DNA molecules are heat-denatured again. In either case the single stranded DNA is made fully double stranded by addition of second target-specific primer, followed by polymerization. The double stranded DNA molecules are then multiply 15 transcribed by a polymerase such as T7 or SP6. In an isothermal cyclic reaction, the RNAs are reverse transcribed into DNA, and transcribed once again with a polymerase such as T7 or SP6. The resulting products, whether truncated or complete, indicate target-specific sequences.

Eur. Pat. Appl. Publ. No. 329,822, incorporated herein by reference in its 20 entirety, disclose a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA), which may be used in accordance with the present invention. The ssRNA is a first template for a first primer oligonucleotide, which is elongated by reverse transcriptase (RNA-dependent DNA polymerase). The RNA is then removed from resulting 25 DNA:RNA duplex by the action of ribonuclease H (RNase H, an RNase specific for RNA in a duplex with either DNA or RNA). The resultant ssDNA is a second template for a second primer, which also includes the sequences of an RNA polymerase promoter (exemplified by T7 RNA polymerase) 5' to its homology to its template. This primer is then extended by DNA polymerase (exemplified by the large "Klenow" 30 fragment of *E. coli* DNA polymerase I), resulting as a double-stranded DNA ("dsDNA") molecule, having a sequence identical to that of the original RNA between

the primers and having additionally, at one end, a promoter sequence. This promoter sequence can be used by the appropriate RNA polymerase to make many RNA copies of the DNA. These copies can then re-enter the cycle leading to very swift amplification. With proper choice of enzymes, this amplification can be done 5 isothermally without addition of enzymes at each cycle. Because of the cyclical nature of this process, the starting sequence can be chosen to be in the form of either DNA or RNA.

PCT Intl. Pat. Appl. Publ. No. WO 89/06700, incorporated herein by reference in its entirety, disclose a nucleic acid sequence amplification scheme based on 10 the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. This scheme is not cyclic; *i.e.* new templates are not produced from the resultant RNA transcripts. Other amplification methods include "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara, 1989) which are well-known to those of skill in the art. 15 Methods based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide (Wu and Dean, 1996, incorporated herein by reference in its entirety), may also be used in the amplification of DNA sequences of the present invention.

20 BIOLOGICAL FUNCTIONAL EQUIVALENTS

Modification and changes may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a polypeptide with desirable characteristics. As mentioned above, it is often desirable to introduce one or more mutations into a specific 25 polynucleotide sequence. In certain circumstances, the resulting encoded polypeptide sequence is altered by this mutation, or in other cases, the sequence of the polypeptide is unchanged by one or more mutations in the encoding polynucleotide.

When it is desirable to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, second-generation molecule, the amino acid

changes may be achieved by changing one or more of the codons of the encoding DNA sequence, according to Table 1.

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with 5 structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus 10 contemplated by the inventors that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

TABLE I

Amino Acids		Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	UGC	UGU				
Aspartic acid	Asp	D	GAC	GAU				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	UUC	UUU				
Glycine	Gly	G	GGA	GGC	GGG	GGU		
Histidine	His	H	CAC	CAU				
Isoleucine	Ile	I	AUA	AUC	AUU			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU
Methionine	Met	M	AUG					
Asparagine	Asn	N	AAC	AAU				
Proline	Pro	P	CCA	CCC	CCG	CCU		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
Threonine	Thr	T	ACA	ACC	ACG	ACU		
Valine	Val	V	GUU	GUC	GUG	GUU		
Tryptophan	Trp	W	UGG					
Tyrosine	Tyr	Y	UAC	UAU				

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring 5 interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and 10 the like. Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are:

isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-5 4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose 10 hydropathic indices are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a 15 protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate ($+3.0 \pm 1$); glutamate ($+3.0 \pm 1$); serine (+0.3); asparagine (+0.2); glutamine 20 (+0.2); glycine (0); threonine (-0.4); proline (-0.5 ± 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In 25 such changes, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their 30 hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that take various of the foregoing characteristics into consideration are well known to those

of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of 5 flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

10 IN VIVO POLYNUCLEOTIDE DELIVERY TECHNIQUES

In additional embodiments, genetic constructs comprising one or more of the polynucleotides of the invention are introduced into cells *in vivo*. This may be achieved using any of a variety of well known approaches, several of which are outlined below for the purpose of illustration.

15 1. ADENOVIRUS

One of the preferred methods for *in vivo* delivery of one or more nucleic acid sequences involves the use of an adenovirus expression vector. "Adenovirus expression vector" is meant to include those constructs containing adenovirus sequences sufficient to (a) support packaging of the construct and (b) to express a 20 polynucleotide that has been cloned therein in a sense or antisense orientation. Of course, in the context of an antisense construct, expression does not require that the gene product be synthesized.

The expression vector comprises a genetically engineered form of an adenovirus. Knowledge of the genetic organization of adenovirus, a 36 kb, linear, 25 double-stranded DNA virus, allows substitution of large pieces of adenoviral DNA with foreign sequences up to 7 kb (Grunhaus and Horwitz, 1992). In contrast to retrovirus, the adenoviral infection of host cells does not result in chromosomal integration because adenoviral DNA can replicate in an episomal manner without potential genotoxicity. Also, adenoviruses are structurally stable, and no genome rearrangement

has been detected after extensive amplification. Adenovirus can infect virtually all epithelial cells regardless of their cell cycle stage. So far, adenoviral infection appears to be linked only to mild disease such as acute respiratory disease in humans.

Adenovirus is particularly suitable for use as a gene transfer vector because of its mid-sized genome, ease of manipulation, high titer, wide target-cell range and high infectivity. Both ends of the viral genome contain 100-200 base pair inverted repeats (ITRs), which are *cis* elements necessary for viral DNA replication and packaging. The early (E) and late (L) regions of the genome contain different transcription units that are divided by the onset of viral DNA replication. The E1 region (E1A and E1B) encodes proteins responsible for the regulation of transcription of the viral genome and a few cellular genes. The expression of the E2 region (E2A and E2B) results in the synthesis of the proteins for viral DNA replication. These proteins are involved in DNA replication, late gene expression and host cell shut-off (Renan, 1990). The products of the late genes, including the majority of the viral capsid proteins, are expressed only after significant processing of a single primary transcript issued by the major late promoter (MLP). The MLP, (located at 16.8 m.u.) is particularly efficient during the late phase of infection, and all the mRNA's issued from this promoter possess a 5'-tripartite leader (TPL) sequence which makes them preferred mRNA's for translation.

In a current system, recombinant adenovirus is generated from homologous recombination between shuttle vector and provirus vector. Due to the possible recombination between two proviral vectors, wild-type adenovirus may be generated from this process. Therefore, it is critical to isolate a single clone of virus from an individual plaque and examine its genomic structure.

Generation and propagation of the current adenovirus vectors, which are replication deficient, depend on a unique helper cell line, designated 293, which was transformed from human embryonic kidney cells by Ad5 DNA fragments and constitutively expresses E1 proteins (Graham *et al.*, 1977). Since the E3 region is dispensable from the adenovirus genome (Jones and Shenk, 1978), the current adenovirus vectors, with the help of 293 cells, carry foreign DNA in either the E1, the D3 or both regions (Graham and Prevec, 1991). In nature, adenovirus can package

approximately 105% of the wild-type genome (Ghosh-Choudhury *et al.*, 1987), providing capacity for about 2 extra kB of DNA. Combined with the approximately 5.5 kB of DNA that is replaceable in the E1 and E3 regions, the maximum capacity of the current adenovirus vector is under 7.5 kB, or about 15% of the total length of the 5 vector. More than 80% of the adenovirus viral genome remains in the vector backbone and is the source of vector-borne cytotoxicity. Also, the replication deficiency of the E1-deleted virus is incomplete. For example, leakage of viral gene expression has been observed with the currently available vectors at high multiplicities of infection (MOI) (Mulligan, 1993).

10 Helper cell lines may be derived from human cells such as human embryonic kidney cells, muscle cells, hematopoietic cells or other human embryonic mesenchymal or epithelial cells. Alternatively, the helper cells may be derived from the cells of other mammalian species that are permissive for human adenovirus. Such cells include, *e.g.*, Vero cells or other monkey embryonic mesenchymal or epithelial cells.

15 As stated above, the currently preferred helper cell line is 293.

Recently, Racher *et al.* (1995) disclosed improved methods for culturing 293 cells and propagating adenovirus. In one format, natural cell aggregates are grown by inoculating individual cells into 1 liter siliconized spinner flasks (Techne, Cambridge, UK) containing 100-200 ml of medium. Following stirring at 40 rpm, the 20 cell viability is estimated with trypan blue. In another format, Fibra-Cel microcarriers (Bibby Sterlin, Stone, UK) (5 g/l) is employed as follows. A cell inoculum, resuspended in 5 ml of medium, is added to the carrier (50 ml) in a 250 ml Erlenmeyer flask and left stationary, with occasional agitation, for 1 to 4 h. The medium is then replaced with 50 ml of fresh medium and shaking initiated. For virus production, cells 25 are allowed to grow to about 80% confluence, after which time the medium is replaced (to 25% of the final volume) and adenovirus added at an MOI of 0.05. Cultures are left stationary overnight, following which the volume is increased to 100% and shaking commenced for another 72 h.

Other than the requirement that the adenovirus vector be replication 30 defective, or at least conditionally defective, the nature of the adenovirus vector is not believed to be crucial to the successful practice of the invention. The adenovirus may

be of any of the 42 different known serotypes or subgroups A-F. Adenovirus type 5 of subgroup C is the preferred starting material in order to obtain a conditional replication-defective adenovirus vector for use in the present invention, since Adenovirus type 5 is a human adenovirus about which a great deal of biochemical and genetic information is 5 known, and it has historically been used for most constructions employing adenovirus as a vector.

As stated above, the typical vector according to the present invention is replication defective and will not have an adenovirus E1 region. Thus, it will be most convenient to introduce the polynucleotide encoding the gene of interest at the position 10 from which the E1-coding sequences have been removed. However, the position of insertion of the construct within the adenovirus sequences is not critical to the invention. The polynucleotide encoding the gene of interest may also be inserted in lieu of the deleted E3 region in E3 replacement vectors as described by Karlsson *et al.* (1986) or in the E4 region where a helper cell line or helper virus complements the E4 15 defect.

Adenovirus is easy to grow and manipulate and exhibits broad host range *in vitro* and *in vivo*. This group of viruses can be obtained in high titers, *e.g.*, 10^9 - 10^{11} plaque-forming units per ml, and they are highly infective. The life cycle of adenovirus does not require integration into the host cell genome. The foreign genes 20 delivered by adenovirus vectors are episomal and, therefore, have low genotoxicity to host cells. No side effects have been reported in studies of vaccination with wild-type adenovirus (Couch *et al.*, 1963; Top *et al.*, 1971), demonstrating their safety and therapeutic potential as *in vivo* gene transfer vectors.

Adenovirus vectors have been used in eukaryotic gene expression 25 (Levrero *et al.*, 1991; Gomez-Foix *et al.*, 1992) and vaccine development (Grunhaus and Horwitz, 1992; Graham and Prevec, 1992). Recently, animal studies suggested that recombinant adenovirus could be used for gene therapy (Stratford-Perricaudet and Perricaudet, 1991; Stratford-Perricaudet *et al.*, 1990; Rich *et al.*, 1993). Studies in administering recombinant adenovirus to different tissues include trachea instillation 30 (Rosenfeld *et al.*, 1991; Rosenfeld *et al.*, 1992), muscle injection (Ragot *et al.*, 1993),

peripheral intravenous injections (Herz and Gerard, 1993) and stereotactic inoculation into the brain (Le Gal La Salle *et al.*, 1993).

2. RETROVIRUSES

The retroviruses are a group of single-stranded RNA viruses characterized by an ability to convert their RNA to double-stranded DNA in infected cells by a process of reverse-transcription (Coffin, 1990). The resulting DNA then stably integrates into cellular chromosomes as a provirus and directs synthesis of viral proteins. The integration results in the retention of the viral gene sequences in the recipient cell and its descendants. The retroviral genome contains three genes, gag, pol, and env that code for capsid proteins, polymerase enzyme, and envelope components, respectively. A sequence found upstream from the gag gene contains a signal for packaging of the genome into virions. Two long terminal repeat (LTR) sequences are present at the 5' and 3' ends of the viral genome. These contain strong promoter and enhancer sequences and are also required for integration in the host cell genome (Coffin, 1990).

In order to construct a retroviral vector, a nucleic acid encoding one or more oligonucleotide or polynucleotide sequences of interest is inserted into the viral genome in the place of certain viral sequences to produce a virus that is replication-defective. In order to produce virions, a packaging cell line containing the gag, pol, and env genes but without the LTR and packaging components is constructed (Mann *et al.*, 1983). When a recombinant plasmid containing a cDNA, together with the retroviral LTR and packaging sequences is introduced into this cell line (by calcium phosphate precipitation for example), the packaging sequence allows the RNA transcript of the recombinant plasmid to be packaged into viral particles, which are then secreted into the culture media (Nicolas and Rubenstein, 1988; Temin, 1986; Mann *et al.*, 1983). The media containing the recombinant retroviruses is then collected, optionally concentrated, and used for gene transfer. Retroviral vectors are able to infect a broad variety of cell types. However, integration and stable expression require the division of host cells (Paskind *et al.*, 1975).

A novel approach designed to allow specific targeting of retrovirus vectors was recently developed based on the chemical modification of a retrovirus by the chemical addition of lactose residues to the viral envelope. This modification could permit the specific infection of hepatocytes *via* sialoglycoprotein receptors.

5 A different approach to targeting of recombinant retroviruses was designed in which biotinylated antibodies against a retroviral envelope protein and against a specific cell receptor were used. The antibodies were coupled *via* the biotin components by using streptavidin (Roux *et al.*, 1989). Using antibodies against major histocompatibility complex class I and class II antigens, they demonstrated the infection
10 of a variety of human cells that bore those surface antigens with an ecotropic virus *in vitro* (Roux *et al.*, 1989).

3. ADENO-ASSOCIATED VIRUSES

AAV (Ridgeway, 1988; Hermonat and Muzychka, 1984) is a parovirus, discovered as a contamination of adenoviral stocks. It is a ubiquitous virus (antibodies
15 are present in 85% of the US human population) that has not been linked to any disease. It is also classified as a dependovirus, because its replication is dependent on the presence of a helper virus, such as adenovirus. Five serotypes have been isolated, of which AAV-2 is the best characterized. AAV has a single-stranded linear DNA that is encapsidated into capsid proteins VP1, VP2 and VP3 to form an icosahedral virion of
20 20 to 24 nm in diameter (Muzychka and McLaughlin, 1988).

The AAV DNA is approximately 4.7 kilobases long. It contains two open reading frames and is flanked by two ITRs (FIG. 2). There are two major genes in the AAV genome: *rep* and *cap*. The *rep* gene codes for proteins responsible for viral replication, whereas *cap* codes for capsid protein VP1-3. Each ITR forms a T-shaped hairpin structure. These terminal repeats are the only essential *cis* components of the AAV for chromosomal integration. Therefore, the AAV can be used as a vector with all viral coding sequences removed and replaced by the cassette of genes for delivery. Three viral promoters have been identified and named p5, p19, and p40, according to their map position. Transcription from p5 and p19 results in production of rep proteins,

and transcription from p40 produces the capsid proteins (Hermonat and Muzyczka, 1984).

There are several factors that prompted researchers to study the possibility of using rAAV as an expression vector. One is that the requirements for 5 delivering a gene to integrate into the host chromosome are surprisingly few. It is necessary to have the 145-bp ITRs, which are only 6% of the AAV genome. This leaves room in the vector to assemble a 4.5-kb DNA insertion. While this carrying capacity may prevent the AAV from delivering large genes, it is amply suited for delivering the antisense constructs of the present invention.

10 AAV is also a good choice of delivery vehicles due to its safety. There is a relatively complicated rescue mechanism: not only wild type adenovirus but also AAV genes are required to mobilize rAAV. Likewise, AAV is not pathogenic and not associated with any disease. The removal of viral coding sequences minimizes immune reactions to viral gene expression, and therefore, rAAV does not evoke an inflammatory 15 response.

4. OTHER VIRAL VECTORS AS EXPRESSION CONSTRUCTS

Other viral vectors may be employed as expression constructs in the present invention for the delivery of oligonucleotide or polynucleotide sequences to a host cell. Vectors derived from viruses such as vaccinia virus (Ridgeway, 1988; 20 Coupar *et al.*, 1988), lentiviruses, polio viruses and herpes viruses may be employed. They offer several attractive features for various mammalian cells (Friedmann, 1989; Ridgeway, 1988; Coupar *et al.*, 1988; Horwitz *et al.*, 1990).

With the recent recognition of defective hepatitis B viruses, new insight 25 was gained into the structure-function relationship of different viral sequences. *In vitro* studies showed that the virus could retain the ability for helper-dependent packaging and reverse transcription despite the deletion of up to 80% of its genome (Horwitz *et al.*, 1990). This suggested that large portions of the genome could be replaced with foreign genetic material. The hepatotropism and persistence (integration) were particularly attractive properties for liver-directed gene transfer. Chang *et al.* (1991) 30 introduced the chloramphenicol acetyltransferase (CAT) gene into duck hepatitis B

virus genome in the place of the polymerase, surface, and pre-surface coding sequences. It was cotransfected with wild-type virus into an avian hepatoma cell line. Culture media containing high titers of the recombinant virus were used to infect primary duckling hepatocytes. Stable CAT gene expression was detected for at least 24 days 5 after transfection (Chang *et al.*, 1991).

5. NON-VIRAL VECTORS

In order to effect expression of the oligonucleotide or polynucleotide sequences of the present invention, the expression construct must be delivered into a cell. This delivery may be accomplished *in vitro*, as in laboratory procedures for 10 transforming cells lines, or *in vivo* or *ex vivo*, as in the treatment of certain disease states. As described above, one preferred mechanism for delivery is *via* viral infection where the expression construct is encapsulated in an infectious viral particle.

Once the expression construct has been delivered into the cell the nucleic acid encoding the desired oligonucleotide or polynucleotide sequences may be 15 positioned and expressed at different sites. In certain embodiments, the nucleic acid encoding the construct may be stably integrated into the genome of the cell. This integration may be in the specific location and orientation *via* homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the nucleic acid may be 20 stably maintained in the cell as a separate, episomal segment of DNA. Such nucleic acid segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. How the expression construct is delivered to a cell and where in the cell the nucleic acid remains is dependent on the type of expression construct employed.

25 In certain embodiments of the invention, the expression construct comprising one or more oligonucleotide or polynucleotide sequences may simply consist of naked recombinant DNA or plasmids. Transfer of the construct may be performed by any of the methods mentioned above which physically or chemically permeabilize the cell membrane. This is particularly applicable for transfer *in vitro* but 30 it may be applied to *in vivo* use as well. Dubensky *et al.* (1984) successfully injected

polyomavirus DNA in the form of calcium phosphate precipitates into liver and spleen of adult and newborn mice demonstrating active viral replication and acute infection. Benvenisty and Reshef (1986) also demonstrated that direct intraperitoneal injection of calcium phosphate-precipitated plasmids results in expression of the transfected genes.

5 It is envisioned that DNA encoding a gene of interest may also be transferred in a similar manner *in vivo* and express the gene product.

Another embodiment of the invention for transferring a naked DNA expression construct into cells may involve particle bombardment. This method depends on the ability to accelerate DNA-coated microprojectiles to a high velocity 10 allowing them to pierce cell membranes and enter cells without killing them (Klein *et al.*, 1987). Several devices for accelerating small particles have been developed. One such device relies on a high voltage discharge to generate an electrical current, which in turn provides the motive force (Yang *et al.*, 1990). The microprojectiles used have consisted of biologically inert substances such as tungsten or gold beads.

15 Selected organs including the liver, skin, and muscle tissue of rats and mice have been bombarded *in vivo* (Yang *et al.*, 1990; Zelenin *et al.*, 1991). This may require surgical exposure of the tissue or cells, to eliminate any intervening tissue between the gun and the target organ, *i.e. ex vivo* treatment. Again, DNA encoding a particular gene may be delivered *via* this method and still be incorporated by the present 20 invention.

ANTISENSE OLIGONUCLEOTIDES

The end result of the flow of genetic information is the synthesis of protein. DNA is transcribed by polymerases into messenger RNA and translated on the ribosome to yield a folded, functional protein. Thus there are several steps along the 25 route where protein synthesis can be inhibited. The native DNA segment coding for a polypeptide described herein, as all such mammalian DNA strands, has two strands: a sense strand and an antisense strand held together by hydrogen bonding. The messenger RNA coding for polypeptide has the same nucleotide sequence as the sense DNA strand except that the DNA thymidine is replaced by uridine. Thus, synthetic

antisense nucleotide sequences will bind to a mRNA and inhibit expression of the protein encoded by that mRNA.

The targeting of antisense oligonucleotides to mRNA is thus one mechanism to shut down protein synthesis, and, consequently, represents a powerful and targeted therapeutic approach. For example, the synthesis of polygalactauronase and the muscarine type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829, each specifically incorporated herein by reference in its entirety). Further, examples of antisense inhibition have been demonstrated with the 5 nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1, striatal GABA_A receptor and human EGF (Jaskulski *et al.*, 1988; Vasanthakumar and Ahmed, 1989; Peris *et al.*, 1998; U. S. Patent 5,801,154; U. S. Patent 5,789,573; U. S. Patent 5,718,709 and U. S. Patent 5,610,288, each specifically incorporated herein by reference in its entirety). Antisense constructs have also been 10 described that inhibit and can be used to treat a variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S. Patent 5,591,317 and U. S. Patent 5,783,683, each specifically incorporated herein by reference in its entirety).

Therefore, in exemplary embodiments, the invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is 15 capable of specifically binding to polynucleotide sequence described herein, or a complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified 20 DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In 25 each case, preferred compositions comprise a sequence region that is complementary, and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein.

Selection of antisense compositions specific for a given gene sequence is 30 based upon analysis of the chosen target sequence (*i.e.* in these illustrative examples the rat and human sequences) and determination of secondary structure, T_m , binding

energy, relative stability, and antisense compositions were selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell.

Highly preferred target regions of the mRNA, are those which are at or
5 near the AUG translation initiation codon, and those sequences which were substantially complementary to 5' regions of the mRNA. These secondary structure analyses and target site selection considerations were performed using v.4 of the OLIGO primer analysis software (Rychlik, 1997) and the BLASTN 2.0.5 algorithm software (Altschul *et al.*, 1997).

10 The use of an antisense delivery method employing a short peptide vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris *et al.*, 1997). It has been demonstrated that several molecules of the MPG peptide coat the antisense
15 oligonucleotides and can be delivered into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane (Morris *et al.*, 1997).

RIBOZYMES

20 Although proteins traditionally have been used for catalysis of nucleic acids, another class of macromolecules has emerged as useful in this endeavor. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, 1987; Gerlach *et al.*, 1987; Forster and Symons, 1987). For example, a
25 large number of ribozymes accelerate phosphoester transfer reactions with a high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, 1981; Michel and Westhof, 1990; Reinhold-Hurek and Shub, 1992). This specificity has been attributed to the requirement that the substrate bind via specific base-pairing interactions to the internal guide sequence
30 ("IGS") of the ribozyme prior to chemical reaction.

Ribozyme catalysis has primarily been observed as part of sequence-specific cleavage/ligation reactions involving nucleic acids (Joyce, 1989; Cech *et al.*, 1981). For example, U. S. Patent No. 5,354,855 (specifically incorporated herein by reference) reports that certain ribozymes can act as endonucleases with a sequence 5 specificity greater than that of known ribonucleases and approaching that of the DNA restriction enzymes. Thus, sequence-specific ribozyme-mediated inhibition of gene expression may be particularly suited to therapeutic applications (Scanlon *et al.*, 1991; Sarver *et al.*, 1990). Recently, it was reported that ribozymes elicited genetic changes in some cells lines to which they were applied; the altered genes included the oncogenes 10 *H-ras*, *c-fos* and genes of HIV. Most of this work involved the modification of a target mRNA, based on a specific mutant codon that is cleaved by a specific ribozyme.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general, 15 enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to 20 cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many 25 technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of 30 target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding to the target

RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action (Woolf *et al.*, 1992). Thus, the specificity of action of a ribozyme is greater than that of 5 an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis δ virus, group I intron or RNaseP RNA (in association with an RNA guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are described by Rossi *et al.* (1992). Examples of hairpin motifs are described by Hampel 10 *et al.* (Eur. Pat. Appl. Publ. No. EP 0360257), Hampel and Tritz (1989), Hampel *et al.* (1990) and U. S. Patent 5,631,359 (specifically incorporated herein by reference). An example of the hepatitis δ virus motif is described by Perrotta and Been (1992); an example of the RNaseP motif is described by Guerrier-Takada *et al.* (1983); Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, 15 1990; Saville and Collins, 1991; Collins and Olive, 1993); and an example of the Group I intron is described in (U. S. Patent 4,987,071, specifically incorporated herein by reference). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or 20 surrounding that substrate binding site which impart an RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

In certain embodiments, it may be important to produce enzymatic cleaving agents which exhibit a high degree of specificity for the RNA of a desired 25 target, such as one of the sequences disclosed herein. The enzymatic nucleic acid molecule is preferably targeted to a highly conserved sequence region of a target mRNA. Such enzymatic nucleic acid molecules can be delivered exogenously to specific cells as required. Alternatively, the ribozymes can be expressed from DNA or RNA vectors that are delivered to specific cells.

30 Small enzymatic nucleic acid motifs (e.g., of the hammerhead or the hairpin structure) may also be used for exogenous delivery. The simple structure of

these molecules increases the ability of the enzymatic nucleic acid to invade targeted regions of the mRNA structure. Alternatively, catalytic RNA molecules can be expressed within cells from eukaryotic promoters (e.g., Scanlon *et al.*, 1991; Kashani-Sabet *et al.*, 1992; Dropulic *et al.*, 1992; Weerasinghe *et al.*, 1991; Ojwang *et al.*, 1992; 5 Chen *et al.*, 1992; Sarver *et al.*, 1990). Those skilled in the art realize that any ribozyme can be expressed in eukaryotic cells from the appropriate DNA vector. The activity of such ribozymes can be augmented by their release from the primary transcript by a second ribozyme (Int. Pat. Appl. Publ. No. WO 93/23569, and Int. Pat. Appl. Publ. No. WO 94/02595, both hereby incorporated by reference; Ohkawa *et al.*, 10 Taira *et al.*, 1991; and Ventura *et al.*, 1993).

Ribozymes may be added directly, or can be complexed with cationic lipids, lipid complexes, packaged within liposomes, or otherwise delivered to target cells. The RNA or RNA complexes can be locally administered to relevant tissues *ex vivo*, or *in vivo* through injection, aerosol inhalation, infusion pump or stent, with or 15 without their incorporation in biopolymers.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo*, as described. Such ribozymes can also be optimized for delivery. While specific 20 examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

Hammerhead or hairpin ribozymes may be individually analyzed by computer folding (Jaeger *et al.*, 1989) to assess whether the ribozyme sequences fold into the appropriate secondary structure. Those ribozymes with unfavorable 25 intramolecular interactions between the binding arms and the catalytic core are eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity. Generally, at least 5 or so bases on each arm are able to bind to, or otherwise interact with, the target RNA.

Ribozymes of the hammerhead or hairpin motif may be designed to 30 anneal to various sites in the mRNA message, and can be chemically synthesized. The method of synthesis used follows the procedure for normal RNA synthesis as described

in Usman *et al.* (1987) and in Scaringe *et al.* (1990) and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. Average stepwise coupling yields are typically >98%. Hairpin ribozymes may be synthesized in two parts and annealed to reconstruct an 5 active ribozyme (Chowrira and Burke, 1992). Ribozymes may be modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-flouro, 2'-o-methyl, 2'-H (for a review see e.g., Usman and Cedergren, 1992). Ribozymes may be purified by gel electrophoresis using general methods or by high pressure liquid chromatography and resuspended in water.

10 Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see e.g., Int. Pat. Appl. Publ. No. WO 92/07065; Perrault *et al.*, 1990; Pieken *et al.*, 1991; Usman and Cedergren, 1992; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. 15 Pat. Appl. Publ. No. 92110298.4; U. S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

20 Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable 25 nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, 30 subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions

of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Another means of accumulating high concentrations of a ribozyme(s) 5 within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the 10 nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990; Gao and Huang, 1993; Lieber *et al.*, 1993; Zhou *et al.*, 1990). Ribozymes expressed from such promoters can function in mammalian cells (*e.g.* 15 Kashani-Saber *et al.*, 1992; Ojwang *et al.*, 1992; Chen *et al.*, 1992; Yu *et al.*, 1993; L'Huillier *et al.*, 1992; Lisziewicz *et al.*, 1993). Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or 20 adeno-associated vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

Ribozymes may be used as diagnostic tools to examine genetic drift and mutations within diseased cells. They can also be used to assess levels of the target RNA molecule. The close relationship between ribozyme activity and the structure of the target RNA allows the detection of mutations in any region of the molecule which 25 alters the base-pairing and three-dimensional structure of the target RNA. By using multiple ribozymes, one may map nucleotide changes which are important to RNA structure and function *in vitro*, as well as in cells and tissues. Cleavage of target RNAs with ribozymes may be used to inhibit gene expression and define the role (essentially) of specified gene products in the progression of disease. In this manner, other genetic 30 targets may be defined as important mediators of the disease. These studies will lead to better treatment of the disease progression by affording the possibility of combinational

therapies (e.g., multiple ribozymes targeted to different genes, ribozymes coupled with known small molecule inhibitors, or intermittent treatment with combinations of ribozymes and/or other chemical or biological molecules). Other *in vitro* uses of ribozymes are well known in the art, and include detection of the presence of mRNA 5 associated with an IL-5 related condition. Such RNA is detected by determining the presence of a cleavage product after treatment with a ribozyme using standard methodology.

PEPTIDE NUCLEIC ACIDS

In certain embodiments, the inventors contemplate the use of peptide 10 nucleic acids (PNAs) in the practice of the methods of the invention. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, 1997). PNA is able to be utilized in a number methods that traditionally have used RNA or DNA. Often PNA sequences perform better in techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA 15 or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (1997) and is incorporated herein by reference. As such, in certain embodiments, one may prepare PNA sequences that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE- 20 specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal phosphodiester backbone of DNA (Nielsen *et al.*, 1991; Hanvey *et al.*, 1992; Hyrup and Nielsen, 1996; Nielsen, 1996). This chemistry has three important consequences: 25 firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc (Dueholm *et al.*, 1994) or Fmoc (Thomson *et al.*, 1995) protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used 30 (Christensen *et al.*, 1995).

PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*, 1995). The manual protocol lends itself to the production of chemically modified PNAs

5 or the simultaneous synthesis of families of closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this

10 difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed by the purification of PNAs by reverse-phase high-pressure liquid chromatography (Norton *et al.*, 1995) providing yields and purity of product similar to those observed during the synthesis of peptides.

15 Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or

20 for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry. Several studies have made and utilized modifications of PNAs (Norton *et al.*, 1995; Haaima *et al.*, 1996; Stetsenko *et al.*, 1996; Petersen *et al.*, 1995; Ulmann *et al.*, 1996; Koch *et al.*, 1995; Orum *et al.*, 1995; Footer *et al.*, 1996; Griffith *et al.*, 1995; Kremsky *et al.*, 1996; Pardridge *et al.*,

25 1995; Boffa *et al.*, 1995; Landsdorp *et al.*, 1996; Gambacorti-Passerini *et al.*, 1996; Armitage *et al.*, 1997; Seeger *et al.*, 1997; Ruskowski *et al.*, 1997). U.S. Patent No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to therapeutics.

30 In contrast to DNA and RNA, which contain negatively charged linkages, the PNA backbone is neutral. In spite of this dramatic alteration, PNAs

recognize complementary DNA and RNA by Watson-Crick pairing (Egholm *et al.*, 1993), validating the initial modeling by Nielsen *et al.* (1991). PNAs lack 3' to 5' polarity and can bind in either parallel or antiparallel fashion, with the antiparallel mode being preferred (Egholm *et al.*, 1993).

5 Hybridization of DNA oligonucleotides to DNA and RNA is destabilized by electrostatic repulsion between the negatively charged phosphate backbones of the complementary strands. By contrast, the absence of charge repulsion in PNA-DNA or PNA-RNA duplexes increases the melting temperature (T_m) and reduces the dependence of T_m on the concentration of mono- or divalent cations
10 (Nielsen *et al.*, 1991). The enhanced rate and affinity of hybridization are significant because they are responsible for the surprising ability of PNAs to perform strand invasion of complementary sequences within relaxed double-stranded DNA. In addition, the efficient hybridization at inverted repeats suggests that PNAs can
15 recognize secondary structure effectively within double-stranded DNA. Enhanced recognition also occurs with PNAs immobilized on surfaces, and Wang *et al.* have shown that support-bound PNAs can be used to detect hybridization events (Wang *et al.*, 1996).

One might expect that tight binding of PNAs to complementary sequences would also increase binding to similar (but not identical) sequences, reducing
20 the sequence specificity of PNA recognition. As with DNA hybridization, however, selective recognition can be achieved by balancing oligomer length and incubation temperature. Moreover, selective hybridization of PNAs is encouraged by PNA-DNA hybridization being less tolerant of base mismatches than DNA-DNA hybridization. For example, a single mismatch within a 16 bp PNA-DNA duplex can reduce the T_m by
25 up to 15°C (Egholm *et al.*, 1993). This high level of discrimination has allowed the development of several PNA-based strategies for the analysis of point mutations (Wang *et al.*, 1996; Carlsson *et al.*, 1996; Thiede *et al.*, 1996; Webb and Hurskainen, 1996; Perry-O'Keefe *et al.*, 1996).

High-affinity binding provides clear advantages for molecular
30 recognition and the development of new applications for PNAs. For example, 11-13 nucleotide PNAs inhibit the activity of telomerase, a ribonucleo-protein that extends

telomere ends using an essential RNA template, while the analogous DNA oligomers do not (Norton *et al.*, 1996).

Neutral PNAs are more hydrophobic than analogous DNA oligomers, and this can lead to difficulty solubilizing them at neutral pH, especially if the PNAs 5 have a high purine content or if they have the potential to form secondary structures. Their solubility can be enhanced by attaching one or more positive charges to the PNA termini (Nielsen *et al.*, 1991).

Findings by Allfrey and colleagues suggest that strand invasion will occur spontaneously at sequences within chromosomal DNA (Boffa *et al.*, 1995; Boffa 10 *et al.*, 1996). These studies targeted PNAs to triplet repeats of the nucleotides CAG and used this recognition to purify transcriptionally active DNA (Boffa *et al.*, 1995) and to inhibit transcription (Boffa *et al.*, 1996). This result suggests that if PNAs can be delivered within cells then they will have the potential to be general sequence-specific regulators of gene expression. Studies and reviews concerning the use of PNAs as 15 antisense and anti-gene agents include Nielsen *et al.* (1993b), Hanvey *et al.* (1992), and Good and Nielsen (1997). Koppelhus *et al.* (1997) have used PNAs to inhibit HIV-1 inverse transcription, showing that PNAs may be used for antiviral therapies.

Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (1993) and Jensen *et al.* (1997). Rose uses capillary gel 20 electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the relative binding kinetics and stoichiometry. Similar types of measurements were made by Jensen *et al.* using BIAcoreTM technology.

Other applications of PNAs include use in DNA strand invasion (Nielsen *et al.*, 1991), antisense inhibition (Hanvey *et al.*, 1992), mutational analysis (Orum *et* 25 *al.*, 1993), enhancers of transcription (Mollegaard *et al.*, 1994), nucleic acid purification (Orum *et al.*, 1995), isolation of transcriptionally active genes (Boffa *et al.*, 1995), blocking of transcription factor binding (Vickers *et al.*, 1995), genome cleavage (Veselkov *et al.*, 1996), biosensors (Wang *et al.*, 1996), *in situ* hybridization (Thisted *et* *al.*, 1996), and in a alternative to Southern blotting (Perry-O'Keefe, 1996).

POLYPEPTIDE COMPOSITIONS

The present invention, in other aspects, provides polypeptide compositions. Generally, a polypeptide of the invention will be an isolated polypeptide (or an epitope, variant, or active fragment thereof) derived from a mammalian species.

5 Preferably, the polypeptide is encoded by a polynucleotide sequence disclosed herein or a sequence which hybridizes under moderately stringent conditions to a polynucleotide sequence disclosed herein. Alternatively, the polypeptide may be defined as a polypeptide which comprises a contiguous amino acid sequence from an amino acid sequence disclosed herein, or which polypeptide comprises an entire amino acid

10 sequence disclosed herein.

In the present invention, a polypeptide composition is also understood to comprise one or more polypeptides that are immunologically reactive with antibodies generated against a polypeptide of the invention, particularly a polypeptide having the amino acid sequence disclosed in SEQ ID NO:126, or to active fragments, or to variants

15 or biological functional equivalents thereof.

Likewise, a polypeptide composition of the present invention is understood to comprise one or more polypeptides that are capable of eliciting antibodies that are immunologically reactive with one or more polypeptides encoded by one or more contiguous nucleic acid sequences contained in SEQ ID NO:1-125, or to active

20 fragments, or to variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency. Particularly illustrative polypeptides include the amino acid sequence disclosed in SEQ ID NO:126.

As used herein, an active fragment of a polypeptide includes a whole or

25 a portion of a polypeptide which is modified by conventional techniques, *e.g.*, mutagenesis, or by addition, deletion, or substitution, but which active fragment exhibits substantially the same structure function, antigenicity, etc., as a polypeptide as described herein.

In certain illustrative embodiments, the polypeptides of the invention

30 will comprise at least an immunogenic portion of a breast tumor protein or a variant thereof, as described herein. As noted above, a "breast tumor protein" is a protein that

is expressed by breast tumor cells. Proteins that are breast tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with breast cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be 5 present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid 10 residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a breast tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera 20 and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native breast tumor protein is a 25 portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary 30 skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be

immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ^{125}I -labeled Protein A.

As noted above, a composition may comprise a variant of a native breast tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native breast tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (e.g., 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

Polypeptide variants encompassed by the present invention include those exhibiting at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity (determined as described above) to the polypeptides disclosed herein.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and

alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain

5 nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

10 As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support.

15 For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any

20 appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells, such as mammalian cells and plant cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which

25 secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

30 Portions and other variants having less than about 100 amino acids, and generally less than about 50 amino acids, may also be generated by synthetic means,

using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. *See Merrifield, J. Am. Chem. Soc.* 5 *85*:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion 10 protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than 15 the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

20 Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression 25 vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

30 A peptide linker sequence may be employed to separate the first and second polypeptide components by a distance sufficient to ensure that each polypeptide

folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a 5 secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as 10 linkers include those disclosed in Maratea *et al.*, *Gene* 40:39-46, 1985; Murphy *et al.*, *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to 15 separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and 20 transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided. Such proteins comprise a polypeptide as described herein together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such 25 proteins include tetanus, tuberculosis and hepatitis proteins (see, for example, Stoute *et al. New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenzae* B (WO 91/18926). Preferably, a protein D derivative comprises 30 approximately the first third of the protein (e.g., the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred

embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells.

5 Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is 10 derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the LytA gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This 15 property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (see *Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C- 20 terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is 25 isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a breast tumor protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a breast tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a breast tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as breast cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a breast tumor protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent.

For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an

antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation 5 of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the 10 immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled 15 periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. 20 Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a 25 myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, 30 aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture

supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the 5 yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process 10 in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, 15 *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, 20 differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ⁹⁰Y, ¹²³I, ¹²⁵I, ¹³¹I, ¹⁸⁶Re, ¹⁸⁸Re, ²¹¹At, and ²¹²Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed 25 antiviral protein.

A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such 30 as an amino or sulphhydryl group, on one may be capable of reacting with a carbonyl-

containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, e.g., U.S. Patent No. 4,671,958, to Rodwell *et al.*

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (e.g., U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (e.g., U.S. Patent No. 4,625,014, to Senter *et al.*), by hydrolysis of derivatized amino acid side chains (e.g., U.S. Patent No. 4,638,045, to Kohn *et al.*), by serum complement-mediated hydrolysis (e.g., U.S. Patent No. 4,671,958, to Rodwell *et al.*), and acid-catalyzed hydrolysis (e.g., U.S. Patent No. 4,569,789, to Blattler *et al.*).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be

coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as 5 albumins (e.g., U.S. Patent No. 4,507,234, to Kato *et al.*), peptides and polysaccharides such as aminodextran (e.g., U.S. Patent No. 4,699,784, to Shih *et al.*). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (e.g., U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for 10 radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For 15 example, U.S. Patent No. 4,673,562, to Davison *et al.* discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the 20 antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a breast tumor protein. Such cells may generally be prepared *in vitro* 25 or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine, CA; see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO

92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a breast tumor polypeptide, polynucleotide encoding a breast tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a breast tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

10 T cells are considered to be specific for a breast tumor polypeptide if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two 15 fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen *et al.*, *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by 20 pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a breast tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above 25 for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN- γ) is indicative of T cell activation (see Coligan *et al.*, *Current Protocols in Immunology*, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a breast tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4 $^{+}$ and/or CD8 $^{+}$. Breast tumor protein-specific T cells may 30 be expanded using standard techniques. Within preferred embodiments, the T cells are

derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a breast tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a breast tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a breast tumor polypeptide.

10 Alternatively, one or more T cells that proliferate in the presence of a breast tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

PHARMACEUTICAL COMPOSITIONS

In additional embodiments, the present invention concerns formulation 15 of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions disclosed herein in pharmaceutically-acceptable solutions for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

It will also be understood that, if desired, the nucleic acid segment, RNA, DNA or PNA compositions that express a polypeptide as disclosed herein may be 20 administered in combination with other agents as well, such as, *e.g.*, other proteins or polypeptides or various pharmaceutically-active agents. In fact, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in 25 the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

Formulation of pharmaceutically-acceptable excipients and carrier 30 solutions is well-known to those of skill in the art, as is the development of suitable

dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including *e.g.*, oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation.

1. ORAL DELIVERY

5 In certain applications, the pharmaceutical compositions disclosed herein may be delivered *via* oral administration to an animal. As such, these compositions may be formulated with an inert diluent or with an assimilable edible carrier, or they may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

10 The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs, suspensions, syrups, wafers, and the like (Mathiowitz *et al.*, 1997; Hwang *et al.*, 1998; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451, each specifically incorporated herein by reference in its entirety). The tablets, troches, pills, 15 capsules and the like may also contain the following: a binder, as gum tragacanth, acacia, cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry 20 flavoring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. A syrup or elixir may contain the active compound sucrose as a sweetening agent methyl and 25 propylparabens as preservatives, a dye and flavoring, such as cherry or orange flavor. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds may be incorporated into sustained-release preparation and formulations.

Typically, these formulations may contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or 70% or more of the weight or volume of the total formulation. Naturally, the amount of active compound(s) in each therapeutically useful composition may be prepared in such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of dosages and treatment regimens may be desirable.

For oral administration the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. For example, a mouthwash may be prepared incorporating the active ingredient in the required amount in an appropriate solvent, such as a sodium borate solution (Dobell's Solution). Alternatively, the active ingredient may be incorporated into an oral solution such as one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants. Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

2. INJECTABLE DELIVERY

In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even intraperitoneally as described in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and U. S. Patent 5,399,363 (each specifically incorporated herein by reference in its entirety). Solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of

storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (U. S. Patent 5,466,468, specifically incorporated herein by reference in its entirety). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

For parenteral administration in an aqueous solution, for example, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event,

determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

Sterile injectable solutions are prepared by incorporating the active 5 compounds in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the 10 preparation of sterile injectable solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

The compositions disclosed herein may be formulated in a neutral or salt 15 form. Pharmaceutically-acceptable salts, include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, 20 ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms such as injectable solutions, drug-release capsules, and the like.

25 As used herein, "carrier" includes any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active 30 ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

The phrase "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human. The preparation of an aqueous composition that contains a protein as an active ingredient is well understood in the art. Typically, such 5 compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared. The preparation can also be emulsified.

3. NASAL DELIVERY

In certain embodiments, the pharmaceutical compositions may be 10 delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, nucleic acids, and peptide compositions directly to the lungs *via* nasal aerosol sprays has been described *e.g.*, in U. S. Patent 5,756,353 and U. S. Patent 5,804,212 (each specifically incorporated herein by reference in its entirety). Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.*, 15 1998) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871, specifically incorporated herein by reference in its entirety) are also well-known in the pharmaceutical arts. Likewise, transmucosal drug delivery in the form of a polytetrafluoroethylene support matrix is described in U. S. Patent 5,780,045 (specifically incorporated herein by reference in its entirety).

20 4. LIPOSOME-, NANOCAPSULE-, AND MICROPARTICLE-MEDIATED DELIVERY

In certain embodiments, the inventors contemplate the use of liposomes, 25 nanocapsules, microparticles, microspheres, lipid particles, vesicles, and the like, for the introduction of the compositions of the present invention into suitable host cells. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like.

Such formulations may be preferred for the introduction of pharmaceutically-acceptable formulations of the nucleic acids or constructs disclosed herein. The formation and use of liposomes is generally known to those of skill in the

art (see for example, Couvreur *et al.*, 1977; Couvreur, 1988; Lasic, 1998; which describes the use of liposomes and nanocapsules in the targeted antibiotic therapy for intracellular bacterial infections and diseases). Recently, liposomes were developed with improved serum stability and circulation half-times (Gabizon and 5 Papahadjopoulos, 1988; Allen and Choun, 1987; U. S. Patent 5,741,516, specifically incorporated herein by reference in its entirety). Further, various methods of liposome and liposome like preparations as potential drug carriers have been reviewed (Takakura, 1998; Chandran *et al.*, 1997; Margalit, 1995; U. S. Patent 5,567,434; U. S. Patent 5,552,157; U. S. Patent 5,565,213; U. S. Patent 5,738,868 and U. S. Patent 5,795,587, 10 each specifically incorporated herein by reference in its entirety).

Liposomes have been used successfully with a number of cell types that are normally resistant to transfection by other procedures including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, 1990; Muller *et al.*, 1990). In addition, liposomes are free of the DNA length constraints that are typical of 15 viral-based delivery systems. Liposomes have been used effectively to introduce genes, drugs (Heath and Martin, 1986; Heath *et al.*, 1986; Balazssovits *et al.*, 1989; Fresta and Puglisi, 1996), radiotherapeutic agents (Pikul *et al.*, 1987), enzymes (Imaizumi *et al.*, 1990a; Imaizumi *et al.*, 1990b), viruses (Faller and Baltimore, 1984), transcription factors and allosteric effectors (Nicolau and Gersonde, 1979) into a variety of cultured 20 cell lines and animals. In addition, several successful clinical trials examining the effectiveness of liposome-mediated drug delivery have been completed (Lopez-Berestein *et al.*, 1985a; 1985b; Coune, 1988; Sculier *et al.*, 1988). Furthermore, several studies suggest that the use of liposomes is not associated with autoimmune responses, toxicity or gonadal localization after systemic delivery (Mori and Fukatsu, 1992).

25 Liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs). MLVs generally have diameters of from 25 nm to 4 μ m. Sonication of MLVs results in the formation of small unilamellar vesicles (SUVs) with diameters in the range of 200 to 500 \AA , containing an aqueous 30 solution in the core.

Liposomes bear resemblance to cellular membranes and are contemplated for use in connection with the present invention as carriers for the peptide compositions. They are widely suitable as both water- and lipid-soluble substances can be entrapped, *i.e.* in the aqueous spaces and within the bilayer itself, respectively. It is 5 possible that the drug-bearing liposomes may even be employed for site-specific delivery of active agents by selectively modifying the liposomal formulation.

In addition to the teachings of Couvreur *et al.* (1977; 1988), the following information may be utilized in generating liposomal formulations. Phospholipids can form a variety of structures other than liposomes when dispersed in 10 water, depending on the molar ratio of lipid to water. At low ratios the liposome is the preferred structure. The physical characteristics of liposomes depend on pH, ionic strength and the presence of divalent cations. Liposomes can show low permeability to ionic and polar substances, but at elevated temperatures undergo a phase transition which markedly alters their permeability. The phase transition involves a change from 15 a closely packed, ordered structure, known as the gel state, to a loosely packed, less-ordered structure, known as the fluid state. This occurs at a characteristic phase-transition temperature and results in an increase in permeability to ions, sugars and drugs.

In addition to temperature, exposure to proteins can alter the 20 permeability of liposomes. Certain soluble proteins, such as cytochrome c, bind, deform and penetrate the bilayer, thereby causing changes in permeability. Cholesterol inhibits this penetration of proteins, apparently by packing the phospholipids more tightly. It is contemplated that the most useful liposome formations for antibiotic and 25 inhibitor delivery will contain cholesterol.

The ability to trap solutes varies between different types of liposomes. For example, MLVs are moderately efficient at trapping solutes, but SUVs are 30 extremely inefficient. SUVs offer the advantage of homogeneity and reproducibility in size distribution, however, and a compromise between size and trapping efficiency is offered by large unilamellar vesicles (LUVs). These are prepared by ether evaporation and are three to four times more efficient at solute entrapment than MLVs.

In addition to liposome characteristics, an important determinant in entrapping compounds is the physicochemical properties of the compound itself. Polar compounds are trapped in the aqueous spaces and nonpolar compounds bind to the lipid bilayer of the vesicle. Polar compounds are released through permeation or when the 5 bilayer is broken, but nonpolar compounds remain affiliated with the bilayer unless it is disrupted by temperature or exposure to lipoproteins. Both types show maximum efflux rates at the phase transition temperature.

Liposomes interact with cells *via* four different mechanisms: endocytosis by phagocytic cells of the reticuloendothelial system such as macrophages 10 and neutrophils; adsorption to the cell surface, either by nonspecific weak hydrophobic or electrostatic forces, or by specific interactions with cell-surface components; fusion with the plasma cell membrane by insertion of the lipid bilayer of the liposome into the plasma membrane, with simultaneous release of liposomal contents into the cytoplasm; and by transfer of liposomal lipids to cellular or subcellular membranes, or vice versa, 15 without any association of the liposome contents. It often is difficult to determine which mechanism is operative and more than one may operate at the same time.

The fate and disposition of intravenously injected liposomes depend on their physical properties, such as size, fluidity, and surface charge. They may persist in tissues for h or days, depending on their composition, and half lives in the blood range 20 from min to several h. Larger liposomes, such as MLVs and LUVs, are taken up rapidly by phagocytic cells of the reticuloendothelial system, but physiology of the circulatory system restrains the exit of such large species at most sites. They can exit only in places where large openings or pores exist in the capillary endothelium, such as the sinusoids of the liver or spleen. Thus, these organs are the predominate site of 25 uptake. On the other hand, SUVs show a broader tissue distribution but still are sequestered highly in the liver and spleen. In general, this *in vivo* behavior limits the potential targeting of liposomes to only those organs and tissues accessible to their large size. These include the blood, liver, spleen, bone marrow, and lymphoid organs.

Targeting is generally not a limitation in terms of the present invention. 30 However, should specific targeting be desired, methods are available for this to be accomplished. Antibodies may be used to bind to the liposome surface and to direct the

antibody and its drug contents to specific antigenic receptors located on a particular cell-type surface. Carbohydrate determinants (glycoprotein or glycolipid cell-surface components that play a role in cell-cell recognition, interaction and adhesion) may also be used as recognition sites as they have potential in directing liposomes to particular 5 cell types. Mostly, it is contemplated that intravenous injection of liposomal preparations would be used, but other routes of administration are also conceivable.

Alternatively, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (Henry-Michelland 10 *et al.*, 1987; Quintanar-Guerrero *et al.*, 1998; Douglas *et al.*, 1987). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μ m) should be designed using polymers able to be degraded *in vivo*. Biodegradable polyalkyl-cyanoacrylate nanoparticles that meet these requirements are contemplated for use in the present invention. Such particles may be easily made, as described 15 (Couvreur *et al.*, 1980; 1988; zur Muhlen *et al.*, 1998; Zambaux *et al.* 1998; Pinto-Alphandry *et al.*, 1995 and U. S. Patent 5,145,684, specifically incorporated herein by reference in its entirety).

VACCINES

In certain preferred embodiments of the present invention, vaccines are 20 provided. The vaccines will generally comprise one or more pharmaceutical compositions, such as those discussed above, in combination with an immunostimulant. An immunostimulant may be any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (e.g., polylactic 25 galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which 30 may be biologically active or inactive. For example, one or more immunogenic

portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

Illustrative vaccines may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch *et al.*, *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner *et al.*, *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner *et al.*, *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld *et al.*, *Science* 252:431-434, 1991; Kolls *et al.*, *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler *et al.*, *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman *et al.*, *Circulation* 88:2838-2848, 1993; and Guzman *et al.*, *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer *et al.*, *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells. It will be apparent that a vaccine may comprise both a polynucleotide and a polypeptide component. Such vaccines may provide for an enhanced immune response.

It will be apparent that a vaccine may contain pharmaceutically acceptable salts of the polynucleotides and polypeptides provided herein. Such salts may be prepared from pharmaceutically acceptable non-toxic bases, including organic bases (e.g., salts of primary, secondary and tertiary amines and basic amino acids) and 5 inorganic bases (e.g., sodium, potassium, lithium, ammonium, calcium and magnesium salts).

While any suitable carrier known to those of ordinary skill in the art may be employed in the vaccine compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may 10 be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, 15 lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268; 5,075,109; 5,928,647; 20 5,811,128; 5,820,883; 5,853,763; 5,814,344 and 5,942,252. One may also employ a carrier comprising the particulate-protein complexes described in U.S. Patent No. 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte 25 responses in a host.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextran), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. 30 Alternatively, compositions of the present invention may be formulated as a

lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a 5 substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck 10 and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as 15 GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, 20 high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level 25 of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-30 de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Corixa Corporation (Seattle, WA; see US Patent

Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5 5,856,462. Immunostimulatory DNA sequences are also described, for example, by Sato *et al.*, *Science* 273:352, 1996. Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the 10 combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

15 Other preferred adjuvants include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (*e.g.*, SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in 20 pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties.

Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient. The compositions described herein may be administered 25 as part of a sustained release formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology (*see, e.g.*, Coombes *et al.*, *Vaccine* 14:1429-1438, 1996) and administered by, for example, oral, rectal or subcutaneous implantation, or by 30 implantation at the desired target site. Sustained-release formulations may contain a

polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane.

Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (e.g., a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (see e.g., U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (i.e., matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (see Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up,

process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As 5 an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel *et al.*, *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph 10 nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into 15 dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" 20 cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high 25 expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (e.g., CD54 and CD11) and costimulatory molecules (e.g., CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a 30 breast tumor protein (or portion or other variant thereof) such that the breast tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such

transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be

5 performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi *et al.*, *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the breast tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant

10 bacterium or viruses (e.g., vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of

15 the polypeptide.

Vaccines and pharmaceutical compositions may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are preferably hermetically sealed to preserve sterility of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a vaccine or pharmaceutical composition may be

20 stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as breast cancer. Within such

25 methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using

30 criteria generally accepted in the art, including the presence of a malignant tumor.

Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. Administration may be by any suitable method, including administration by intravenous, intraperitoneal, 5 intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune 10 response-modifying agents (such as polypeptides and polynucleotides as provided herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or 15 indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and 20 macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive 25 immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture 30 conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above,

immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides 5 or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies 10 have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (see, for example, Cheever *et al.*, *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex* 15 *vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitory, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be 20 readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations 25 may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine- 30 dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that

leads to an improved clinical outcome (e.g., more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose 5 ranges from about 25 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical 10 outcome (e.g., more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a breast tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using 15 samples obtained from a patient before and after treatment.

CANCER DETECTION AND DIAGNOSIS

In general, a cancer may be detected in a patient based on the presence of one or more breast tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies) 20 obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as breast cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level 25 of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a breast tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.,* 30 Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory,

1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

5 In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a
10 binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to
15 which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length breast tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill
20 in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S.
25 Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and
30 functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is

preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or 5 polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with 10 both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at 15 A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. 20 Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

25 More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to 30 bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact

time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with breast cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide.

- 5 Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support 10 with an appropriate buffer, such as PBS containing 0.1% Tween 20TM. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. 15 An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are 20 generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of 25 the reaction products.

To determine the presence or absence of a cancer, such as breast cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average 30 mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three

standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett *et al.*, *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, 5 p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample 10 generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

15 In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution 20 containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. 25 Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the 30 biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above.

Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological 5 sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use 10 breast tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such breast tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a breast tumor protein in a biological sample. Within 15 certain methods, a biological sample comprising CD4 $^{+}$ and/or CD8 $^{+}$ T cells isolated from a patient is incubated with a breast tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. 20 For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (e.g., 5 - 25 μ g/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of breast tumor polypeptide to serve as a control. For CD4 $^{+}$ T cells, 25 activation is preferably detected by evaluating proliferation of the T cells. For CD8 $^{+}$ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

30 As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a breast tumor protein in a biological sample. For

example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a breast tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the breast tumor protein. The amplified 5 cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a breast tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers 10 and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a breast tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a 15 polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule 20 having a sequence recited in SEQ ID NO:1-_____. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in 25 conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and 30 from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-

fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the compositions described herein may be used 5 as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the 10 level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound 15 binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple breast tumor protein markers may be assayed within a given sample. It will be apparent that binding agents 20 specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

25 DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may 30 contain a monoclonal antibody or fragment thereof that specifically binds to a breast

tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable

5 for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a breast tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a breast tumor protein. Such an oligonucleotide may be used,

10 for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a breast tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

IDENTIFICATION OF BREAST TUMOR PROTEIN CDNAS

5 This Example illustrates the identification of cDNA molecules encoding breast tumor proteins.

Potential breast-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatzis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST 10 clones (26,074) derived from various human breast cDNA libraries were obtained from the GenBank public human EST database. Each breast EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (BLAST score > 40, length of matching sequence >100 base pairs, density of identical matches over this 15 region > 80%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 9,974 breast superclusters.

20 Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups, Plus (normal breast and breast tumor libraries, and breast cell lines, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other 25 (fetal tissue, infant tissue, ovary, pregnant uterus, male-specific tissues, non-breast tumors and cell lines other than breast cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table I.

TABLE I**BREAST cDNA LIBRARIES**

Library	# of Libraries
Plus	11
Normal	6
Tumor	4
Cell lines	1
Minus	171
Other	297

Each supercluster was analyzed in terms of the ESTs within the 5 supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1 - EST clones derived from the Plus group libraries only; no EST clones derived from Minus or Other group libraries; Type 2 - EST clones derived from the Plus and Other group libraries only; no EST clones derived from the Minus group; Type 3 - EST clones derived from the Plus, Minus and 10 Other group libraries, but the number of EST clones derived from the Plus group is higher than from either the Minus or Other groups; and Type 4 - EST clones derived from Plus, Minus and Other group libraries, but the number of clones derived from the Plus group is higher than the number from the Minus group. For each type, subcategories were generated for clusters containing one or two clones. Types 1a, 2a, 15 3a and 4a represent Type 1, 2, 3 and 4 clusters where the number of clones in the Plus group is 2. Types 1b, 2b, 3b and 4b represent Type 1, 2, 3 and 4 clusters where the number of clones in the Plus group is 1. This analysis identified 3230 breast clusters. From these clusters, 2501 EST clones were ordered from Research Genetics, Inc. (Huntsville, AL), and were received as frozen glycerol stocks in 96-well plates. A 20 summary of the clusters generated and clones ordered is shown in Table II.

TABLE II**BREAST CLUSTER SUMMARY**

Type	# of Superclusters	# of ESTs Ordered
1	50	49
1a (2/0/0)	130	130
1b (1/0/0)	65	65
2	167	162
2a (2/0/n)	312	321
2a (1/0/n)	1875	1752
3	56	22
3a	32	0
4	333	0
4a	210	0
Total	3230	2501

The EST clone inserts were PCR-amplified for Synteni microarray analysis using amino-linked PCR primers. When more than one PCR product was obtained for a particular clone, that clone was not used for expression analysis. In total, 1896 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor breast cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 2 (i.e., the level in breast tumor cDNA was at least twice the level in normal breast cDNA) were identified as

breast tumor-specific sequences (Table III). The sequences of these clones are provided in SEQ ID NOs:1-124.

TABLE III

5

BREAST-TUMOR SPECIFIC CLONES

SEQ ID NO.	Sequence Designation
1	19702
2	19703
3	B1003C
4	B1002C
5	19708
6	19709
7	19710
8	19711
9	B1006C
10	B1007C
11	19714
12	19715
13	19716
14	19717
15	19718
16	19719
17	19720
18	19721
19	19997
20	19998
21	19999
22	20000
23	20001
24	20002
25	20005
26	20006
27	20007
28	20008
29	20009
30	20010
31	20011
32	20012
33	20013
34	20014

35	20079
36	20080
37	20081
38	20082
39	20083
40	20085
41	20086
42	20087
43	20088
44	20089
45	20090
46	20091
47	20092
48	20093
49	20115
50	20116
51	20118
52	20119
53	20120
54	20121
55	20122
56	20123
57	20124
58	20125
59	20360
60	20361
61	20362
62	22180
63	22181
64	22182
65	22183
66	22185
67	22186
68	22188
69	22189
70	22190
71	22191
72	22192
73	22193
74	22194
75	22196
76	22197
77	22198
78	22199
79	22200
80	22201

81	22202
82	22204
83	22206
84	22207
85	22208
86	22209
87	22210
88	22211
89	22212
90	22213
91	22214
92	22215
93	22216
94	22217
95	22218
96	22219
97	22220
98	22221
99	22222
100	22223
101	22224
102	22225
103	22226
104	22227
105	22228
106	22229
107	22230
108	22231
109	22232
110	22233
111	22234
112	22235
113	22236
114	22237
115	22238
116	22239
117	22240
118	22241
119	22242
120	22243
121	22244
122	22245
123	22334
124	22335

The B1002C sequence (SEQ ID NO:4; 517 bp) was used in a BlastN search of the GenBank Human EST database to identify overlapping sequences that extended further toward the 5' end of the corresponding gene. Two human EST clones were identified in this manner and were purchased from Genome Systems (St. Louis, 5 MO) and sequenced. The resulting sequence information gave rise to a partial predicted open reading frame of 214 amino acids, which is 88% identical over 180 amino acids to the mouse "iroquois homeobox protein 3" (GenBank protein accession #Y15001). The extended B1002C sequence, along with the predicted open reading frame, are provided herein as SEQ ID NOs:125 and 126, respectively. The alignment between B1002C and 10 the mouse iroquois homeobox protein 3 is presented in Figure 1.

EXAMPLE 2

SYNTHESIS OF POLYPEPTIDES

15

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems Division 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a 20 method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 25 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

30

From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is claimed:

1. An isolated polypeptide, comprising at least an immunogenic portion of a breast tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
 - (a) sequences recited in SEQ ID NOS:1, 3, 4, 8, 9, 11, 12, 14, 15, 17, 26, 30, 31, 35, 36, 47, 52, 55, 60, 62, 63, 66, 69, 71, 72, 74-78, 81, 83-87, 92, 94, 97, 99-104, 107, 108, 110, 112, 113, 117, 118, 120-122 or 125;
 - (b) sequences that hybridize to a sequence recited in any one of SEQ ID NOS:1, 3, 4, 8, 9, 11, 12, 14, 15, 17, 26, 30, 31, 35, 36, 47, 52, 55, 60, 62, 63, 66, 69, 71, 72, 74-78, 81, 83-87, 92, 94, 97, 99-104, 107, 108, 110, 112, 113, 117, 118, 120-122 or 125, under moderately stringent conditions; and
 - (c) complements of sequences of (a) or (b).
2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOS:1, 3, 4, 8, 9, 11, 12, 14, 15, 17, 26, 30, 31, 35, 36, 47, 52, 55, 60, 62, 63, 66, 69, 71, 72, 74-78, 81, 83-87, 92, 94, 97, 99-104, 107, 108, 110, 112, 113, 117, 118, 120-122 or 125, or a complement of any of the foregoing polynucleotide sequences.
3. An isolated polypeptide comprising a sequence recited in SEQ ID NO:126.
4. An isolated polynucleotide encoding at least 15 amino acid residues of a breast tumor protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ

ID NOs:1, 3, 4, 8, 9, 11, 12, 14, 15, 17, 26, 30, 31, 35, 36, 47, 52, 55, 60, 62, 63, 66, 69, 71, 72, 74-78, 81, 83-87, 92, 94, 97, 99-104, 107, 108, 110, 112, 113, 117, 118, 120-122 or 125, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a breast tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:1, 3, 4, 8, 9, 11, 12, 14, 15, 17, 26, 30, 31, 35, 36, 47, 52, 55, 60, 62, 63, 66, 69, 71, 72, 74-78, 81, 83-87, 92, 94, 97, 99-104, 107, 108, 110, 112, 113, 117, 118, 120-122 or 125, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide, comprising a sequence recited in any one of SEQ ID NOs: 1, 3, 4, 8, 9, 11, 12, 14, 15, 17, 26, 30, 31, 35, 36, 47, 52, 55, 60, 62, 63, 66, 69, 71, 72, 74-78, 81, 83-87, 92, 94, 97, 99-104, 107, 108, 110, 112, 113, 117, 118, 120-122 or 125.

7. An isolated polynucleotide, comprising a sequence that hybridizes to a sequence recited in any one of SEQ ID NOs:1, 3, 4, 8, 9, 11, 12, 14, 15, 17, 26, 30, 31, 35, 36, 47, 52, 55, 60, 62, 63, 66, 69, 71, 72, 74-78, 81, 83-87, 92, 94, 97, 99-104, 107, 108, 110, 112, 113, 117, 118, 120-122 or 125, under moderately stringent conditions.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector, comprising a polynucleotide according to any one of claims claim 4-8.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a breast tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1, 3, 4, 8, 9, 11, 12, 14, 15, 17, 26, 30, 31, 35, 36, 47, 52, 55, 60, 62, 63, 66, 69, 71, 72, 74-78, 81, 83-87, 92, 94, 97, 99-104, 107, 108, 110, 112, 113, 117, 118, 120-122 or 125, or a complement of any of the foregoing polynucleotide sequences.

12. A fusion protein, comprising at least one polypeptide according to claim 1.

13. A fusion protein according to claim 12, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

14. A fusion protein according to claim 12, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

15. A fusion protein according to claim 12, wherein the fusion protein comprises an affinity tag.

16. An isolated polynucleotide encoding a fusion protein according to claim 12.

17. A pharmaceutical composition, comprising a physiologically acceptable carrier and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to claim 11;
- (d) a fusion protein according to claim 12; and
- (e) a polynucleotide according to claim 16.

18. A vaccine comprising an immunostimulant and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to claim 11;
- (d) a fusion protein according to claim 12; and
- (e) a polynucleotide according to claim 16.

19. A vaccine according to claim 18, wherein the immunostimulant is an adjuvant.

20. A vaccine according to any claim 18, wherein the immunostimulant induces a predominantly Type I response.

21. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 17.

22. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 18.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a breast tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

- (a) sequences recited in SEQ ID NOs:1-125;
- (b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs:1-125 under moderately stringent conditions; and
- (c) complements of sequences of (i) or (ii);
in combination with an immunostimulant.

26. A vaccine according to claim 25, wherein the immunostimulant is an adjuvant.

27. A vaccine according to claim 25, wherein the immunostimulant induces a predominantly Type I response.

28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

29. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a breast tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

- (a) sequences recited in SEQ ID NOs:1-125;
- (b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs:1-125 under moderately stringent conditions; and
- (c) complements of sequences of (i) or (ii) encoded by a polynucleotide recited in any one of SEQ ID NOs:1-125;

and thereby inhibiting the development of a cancer in the patient.

30. A method according to claim 29, wherein the antigen-presenting cell is a dendritic cell.

31. A method according to any one of claims 21, 22 and 29, wherein the cancer is breast cancer.

32. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a breast tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

- (i) polynucleotides recited in any one of SEQ ID NOs:1-125; and
- (ii) complements of the foregoing polynucleotides;

wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the antigen from the sample.

33. A method according to claim 32, wherein the biological sample is blood or a fraction thereof.

34. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 32.

35. A method for stimulating and/or expanding T cells specific for a breast tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

(a) polypeptides comprising at least an immunogenic portion of a breast tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

- (i) sequences recited in SEQ ID NOS:1-125;
- (ii) sequences that hybridize to a sequence recited in any one of SEQ ID NOS:1-125 under moderately stringent conditions; and
- (iii) complements of sequences of (i) or (ii);

(b) polynucleotides encoding a polypeptide of (a); and

(c) antigen presenting cells that express a polypeptide of (a); under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

36. An isolated T cell population, comprising T cells prepared according to the method of claim 35.

37. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 36.

38. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

- (i) polypeptides comprising at least an immunogenic portion of a breast tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
- (1) sequences recited in SEQ ID NOS:1-125;
- (2) sequences that hybridize to a sequence recited in any one of SEQ ID NOS:1-125 under moderately stringent conditions; and

(3) complements of sequences of (1) or (2);
(ii) polynucleotides encoding a polypeptide of (i); and
(iii) antigen presenting cells that expresses a polypeptide of (i);
such that T cells proliferate; and
(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

39. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:
(i) polypeptides comprising at least an immunogenic portion of a breast tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
(1) sequences recited in SEQ ID NOS:1-125;
(2) sequences that hybridize to a sequence recited in any one of SEQ ID NOS:1-125 under moderately stringent conditions; and
(3) complements of sequences of (1) or (2);
(ii) polynucleotides encoding a polypeptide of (i); and
(iii) antigen presenting cells that express a polypeptide of (i);
such that T cells proliferate;
(b) cloning at least one proliferated cell to provide cloned T cells; and
(c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

40. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with a binding agent that binds to a breast tumor protein, wherein the tumor protein comprises an amino acid

sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-125 or a complement of any of the foregoing polynucleotide sequences;

- (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and
- (c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

41. A method according to claim 40, wherein the binding agent is an antibody.

42. A method according to claim 43, wherein the antibody is a monoclonal antibody.

43. A method according to claim 40, wherein the cancer is breast cancer.

44. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

- (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a breast tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-125 or a complement of any of the foregoing polynucleotide sequences;
- (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
- (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
- (d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

45. A method according to claim 44, wherein the binding agent is an antibody.

46. A method according to claim 45, wherein the antibody is a monoclonal antibody.

47. A method according to claim 44, wherein the cancer is a breast cancer.

48. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a breast tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO:1-125 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

49. A method according to claim 48, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

50. A method according to claim 48, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

51. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a breast tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide

sequence recited in any one of SEQ ID NO:1-125 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

52. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

53. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

54. A diagnostic kit, comprising:

- (a) one or more antibodies according to claim 11; and
- (b) a detection reagent comprising a reporter group.

55. A kit according to claim 54, wherein the antibodies are immobilized on a solid support.

56. A kit according to claim 54, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

57. A kit according to claim 54, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

58. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a breast tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1, 3, 4, 8, 9, 11, 12, 14, 15, 17, 26, 30, 31, 35, 36, 47, 52, 55, 60, 62, 63, 66, 69, 71, 72, 74-78, 81, 83-87, 92, 94, 97, 99-104, 107, 108, 110, 112, 113, 117, 118, 120-122 or 125, or a complement of any of the foregoing polynucleotides.

59. A oligonucleotide according to claim 58, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID NOs:1, 3, 4, 8, 9, 11, 12, 14, 15, 17, 26, 30, 31, 35, 36, 47, 52, 55, 60, 62, 63, 66, 69, 71, 72, 74-78, 81, 83-87, 92, 94, 97, 99-104, 107, 108, 110, 112, 113, 117, 118, 120-122 or 125.

60. A diagnostic kit, comprising:

- (a) an oligonucleotide according to claim 59; and
- (b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

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SEQUENCE LISTING

<110> Corixa Corporation
 Mitcham, Jennifer L.
 Jiang, Yuqiu

<120> COMPOSITIONS AND METHODS FOR THE THERAPY
 AND DIAGNOSIS OF BREAST CANCER

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 <141> 2000-06-23

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ggggctccc	tcatagcac	caatgacctt	aagagccctt	ttgaaggaag	actccatctg	360
atgactcaga	gcaagtattt	tttagtgtgt	tattgttatt	agcaagaaaag	agggccataaa	420
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<212> DNA

<213> Homo sapien

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ccagggtaaa	ggcttccagt	tcagcctcag	ttatttttaga	caatctcgcc	atctttaatt	300
tcttagcttc	ctgttctaat	aaatgcacgg	ctttacctt	cctgtcagaa	ataaaccaag	360
gctctaaaag	atgatttccc	ttctgttaact	ccctagagcc	acagttctc	attcctttc	420
ccattatact	tctcacaatt	cagtttctat	gagtttgatc	acctgatttt	ttaacaaaa	480
tatttctaac	gggaatgggt	gggagtgtctg	gtgaaaagag	gtgaaatgtg	gttgtatgag	540

ccaatcatat ttgtgatttt ttaaaaaaaag tttaaaagga aatatctgtt ctgaaacccc	600
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accatattag cgtaccacc	680

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 <213> Homo sapien

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agaaagaaga aagaacaaga agaagaagga agaaaagaag tggaaagaaa gcatgaatag	180
gagtagcttc acaaagatag gagataaccg agaaactgtt ttatgtcat ctctctgtgt	240
aggccacctt gtaagctgtg gcctcagact tacctttat ctgtgtat gctttttac	300
cactattgtg tctgctgtt atgtctttc caggcatgta ctgtgcagg ggtgtccaaat	360
catttagctt ttctgagaca cactggataa acacaaattt tcctgggcca cacgtaaaat	420
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<210> 4
 <211> 517
 <212> DNA
 <213> Homo sapien

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ttaaaaaaaa caaaaaaaca aaaaaaactt ttttaatcg ttgtataat tgtataaaaa	180
aaatcgctct gtatagttac aacttgcgtg catgtccgtg tataaatacc taaaagcaaa	240
actaaaacaaa gaaagtaaga aaaagaaaata aaaccagtcc tcctcagccc tccccaaagtc	300
gtttctgtgg caccggcat tcgctgtgag gtttgtttgt ccgttgatt ttggggggtg	360
gagtttcagt gagaataaac gtgtctgcct ttgtgtgtgt gtatataac agagaaaatgt	420
acatatgtgt gaaccaatt gtacgagaaa gtatctat ttggctaaat aaatgagctg	480
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 <212> DNA
 <213> Homo sapien

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caaattcagt caccatgtt atattaccc ctccaggaac cttccagtgg ggaaggctgc	180
gatatttagat tcccttgcata gaaaaatgg tttgaaagc tgcgtcaga ggaggtgaga	240
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<210> 6
 <211> 88
 <212> DNA
 <213> Homo sapien

<211> 811
<212> DNA
<213> *Homo sapien*

<400> 9

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cagccaaacac cgagtgtacg tggaccatca accccaccccc caagcgccgc atccctgateg	180
tggtccctga gatcttcctg cccatagagg acgactgtgg ggactatctg gtgatgcgga	240
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tcgccttcac ctccagggtca aagaagctgt ggattcagtt caagtccaaat gaagggaaaca	360
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aagacatagt tcgagatggc aggctctatg catctgagaa ccatcaggaa atacttaagg	480
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acacagccca ggagtccccga gagatgttcc caagatcggtt catccgattt ctacgttcca	600
aagtgtccag gtttttgaga ccttacaat gactcagccc acgtgccact caatacaaat	660
gttctgtat aggggttggtg ggacagagct gtcttccctc tgcatgtcag cacagtccggg	720
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<210> 10

<211> 542

<212> DNA

<213> *Homo sapien*

<220>

<221> misc feature

<222> (1) . . . (542)

<223> n = A, T, C or G

<400> 10

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ctgcaggcata	gaaggggtta	aaagtggaat	gtatgttgc	atagaagttt	aaggttgcaac	180
tcaagaagggaa	aaagaaataaa	cctgtcgaaag	ttatctgtatg	acaaaattacg	aaagtgtctcc	240
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ggaggtatcaa	gagaagttaa	aagcaataga	acccaaatgac	tatacaggaa	aggtctcaga	360
agaaaattgaa	gacatcatca	aaaagggggaa	aacacaaaact	ctttagaaca	taacagaata	420
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gggggatctc	cacgtttgat	ccatTTTcag	cagtgtctgt	aaggaggatatc	ttacttgggt	540
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<210> 11

<211> 508

<212> DNA

<213> Homo sapien

<400> 11

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catgggggag	gctgccacag	gtcacactcc	ttagccggat	cccccctctga	agaaaaagcat	180
ctgagctgac	cagcggagact	gcagtggggc	agacactatt	aaatttgtctg	gcacagctct	240
gagttacccccc	tegettccac	cctgacttca	tcccgagta	gctctcagcc	ctcccaagcccc	300
ctgcagggcc	acgtctttct	ctattggccgg	tcagcgtgtg	tgtgcacaaa	gccccctaagg	360
tttcatgtgt	acacacccgg	gctaagtgtt	ttttacaccc	tttgtcatact	ctcgccctgg	420

ggctcctgtg cagggtcccc tgagagttgg gtttttagtt caaaaagaag gaacacagat
 gactactctg ctggcgacac ggccacta 508

<210> 12
 <211> 836
 <212> DNA
 <213> Homo sapien

<400> 12

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<210> 13
 <211> 530
 <212> DNA
 <213> Homo sapien

<400> 13

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<210> 14
 <211> 809
 <212> DNA
 <213> Homo sapien

<220>
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 <222> (1)...(809)
 <223> n = A,T,C or G

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gcttcaagct	ggctccagac	cactcaaggc	ctccccagcc	tgttcgtcaa	gttgtcctca	360
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 <212> DNA
 <213> Homo sapien

<400> 15						
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atttatcttg	tacatatgt	ttttgaaatc	ttttaaacct	gaaaataaaa	tagtcatttt	840
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 <212> DNA
 <213> Homo sapien

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 <213> Homo sapien

<400> 17

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<210> 22
<211> 576
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<213> *Homo sapien*

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ggaccatatt ctgcggccatc ttctgttctt gggacctgcc agcaccgttt ttgtgttag	180	
ctcccttcttg ccaaccaacc atgagctccc agattegtca gaattattcc accgacgtgg	240	
aggcagccgt caacagccctg gtcaatttgt acctgcaggc ctctcacacc taccttcttc	300	
ttggcttcta ttctggaccc cgatgatgtg gctctggaaag gcgtgagcca ttcttcgc	360	

gaactggccg aggagaagcg cgagggctac gagcgtctcc tgaagatgca aaacca 416

<210> 24

<211> 1037

<212> DNA

<213> *Homo sapien*

<400> 24

gctttaccta	tgggggttgt	tatggcaaca	agaacaacctt	tgaggaagag	cwttagtgcc	60
tcgagtcttg	tgcggcata	tccattaagg	atgtgtttgg	cctgaggccgg	gaaatccccca	120
ttccccagcac	aggctctgtg	gagatggctg	tgcagtgtt	cctggctatc	tgcattgtgg	180
tgggtggtagc	catcttgggt	tactgctct	tcaagaaccac	gagaaaaggac	ttccacggac	240
accaccacca	cccaccaccc	acccttgcac	gctccactgt	ctccactacc	gaggacacgg	300
agcaccttgt	ctataaccac	accacccggc	ccctctgagc	ctgggtctca	ccggctctca	360
cctggccctg	cttcctgttt	gccaaggccag	aggcctgggc	tggaaaaaac	tttggaaacca	420
gactcttgc	tgtttccag	gcccactgtg	cctcagagac	cagggtctca	gcccccttttgc	480
gagaagtctc	agctaagctc	acgtccctgag	aaagctcaaa	ggtttggaaag	gaggcagaaaa	540
cccttggccc	agaagtacca	gactagatgg	acctgcctgc	ataggagttt	ggaggaagtt	600
ggagttttgt	ttcctctgtt	caaagctgcc	tgtccctacc	ccatgggtct	aggaagagga	660
gtgggggtgt	gtcagaccct	ggaggccccca	accctgtctt	cccgagctcc	tyttccatgc	720
tgtgcgcaca	gggctgggag	gaaggacttc	cctgtgtagt	ttgtgtctta	aagagttgtct	780
ttttgtttat	ttaatgtgt	ggcatgggtg	aaggaggaggg	gaagaggccct	gtttggcccty	840
tytgcctyt	yttcctttc	ccccaaagatt	gagctytytg	cccttgatca	gccccccccct	900
ggcctagacc	agcagacaga	gccaggagag	gstcagctgc	attccgcagc	cccccccccccc	960
aaggtttcc	aacatcacag	cccagccac	ccactggta	ataaaaagtgg	tttggaaaaaa	1020
aaaaaaaaaa	aaaaaaaaaa					1037

<210> 25

<211> 1144

<212> DNA

<213> Homo sapien

<400> 25

cggcacagg	ctagatgggt	ccatgacaat	ggtgtgaact	acaagattgg	agagaagtgg	60
gaccgtcagg	gagaaaatgg	ccakatgt	agctgcacat	gtcttgggaa	cggaaaaggaa	120
gaattcaagt	gtgaccctca	tgaggcaacg	tgttacgt	atggggaaagac	ataccacgt	180
ggagaacagt	ggcagaagga	atatctcggt	gccattgct	cctgcacatg	ctttggaggc	240
cagcgggct	ggcgctgtga	caactgccgc	agacctgggg	gtgaacccag	tcccgaaaggc	300
actactggcc	agtccctacaa	ccagttatct	cagagatacc	atcagagaac	aaacactaat	360
gttaattgcc	caattgagtg	cttcatgcct	ttagatgtac	aggctgacag	agaagattcc	420
cgagagtaaa	tcatcttcc	aatccagagg	aacaagcatg	tctctctgccc	aagatccatc	480
taaactggag	tgatgttage	agacccagct	tagagttctt	ctttctttct	taagcccttt	540
gctctggagg	aagtctcca	gcttcagctc	aactcacagc	ttctccaagc	atcacccctgg	600
gagtttctg	agggttttct	cataaatgag	ggctgcacat	tgctctgttct	gcttcgaagt	660
attcaataacc	gctcagtatt	ttaaatgaag	tgattctaag	atttggtttg	ggatcaatag	720
gaaagcatat	gcagccaaacc	aagatgaaa	tgtttgaaa	tgatatgacc	aaaattttaa	780
gtaggaaaagt	cacccaaaca	cttctgttt	cacttaagt	tytggcccg	aatactgtag	840
gaacaaggcat	gatcttgtta	ctgtgtat	ttaaatatcc	mcagtactca	cttttccaa	900
atgatcttag	taattgccta	gaaatatctt	tctcttacct	gttattttatc	aattttcccc	960
agtattttta	tacggaaaaa	attgtattga	aaacmcttag	tatgcagtt	ataagaggaa	1020
tttggtataa	ttatgggggg	tggaaatttt	ttatactgt	tgtccaaag	ctttaaaact	1080
gtggaaagac	aactgtttta	ataaaagatt	tacattcccc	aacttgaaaa	aaaaaaaaaa	1140
aaaa						1144

<210> 26

<211> 488
 <212> DNA
 <213> Homo sapien

<400> 26

gcattttgt ctgtgtctcc ttagtcttcag gtcaccacca tgaagttttt agcagtcttg	60
gtacttgg gagtttccat cttytggtc tctgcccaga atccgacaac agctgctcca	120
gctgacacgt atccagctac tggtctgtct gatgatgaag cccctgtatgc tgaaaccact	180
gctgctgcaa ccactgctgac cactgctgtct cttaccactg caaccaccgc tgcttctacc	240
actgctcgta aagacattcc agttttaccc aaatgggttg gggatctccc gaatggtaga	300
gtgtgtccct gagatggaaat cagcttgagt cttctgcaat tggtcacaac tattcatgtct	360
tcctgtgatt tcatccaact acttaccttgc cttacgatata cccctttatc tctaatacgat	420
ttatTTTt tcaaataaaa aataactatg agcaacataaa aaaaaaaaaa aaaaaaaaaa	480
aaaaaaaaaa	488

<210> 27

<211> 764

<212> DNA

<213> Homo sapien

<400> 27

agccccaggt gagattgcag ctggtgattt attgagaaaac ttccagggttg agtaggccttc	60
attcagggca tgcctctccccc ccaggccccca tcttcataca cttccgcataa gatggccaca	120
attcatcccc cttcatgtgc agctgaaaaa accctgacat tggctcccg tggccggcat	180
acctggcatt gcccactgccc atctctgtga tgaggaattt aacaccagat ctctggcagc	240
tcttgaggaa ttggccagtg gccattctca ggggtgtgtt ctatgtttcc cagagccccg	300
ccaagggtcc ggcacccgtg gcagagccggg gaggttcccc cactctaaag cctactcctt	360
ctctctctag cctcttcagg aggtgggttg agcagcagca atttccacat caatgttagaa	420
gagtcaagtgg atggacaggt ggttttttcc cacaagagag aaatytaagt gtctattgca	480
ggagaaaacgt cccttgcac tccccactct catcaggcca agtggaggac tggccagagg	540
gcctgcacat gcaaaactcca gtcctgcct tcagagagct gaaaagggtc cctcggtctt	600
ttatTTcagg gctttgcattt cgtcttattt cccctctgccc tctcccccgg tttttggag	660
caaggagatg cagctgtatt gtgtacaag ctcatTTtta cagtgtctgt tcatgtataa	720
aagaattact ttcccttttcaaaaaaaaaaaaaaaa aaaaaaaa	764

<210> 28

<211> 802

<212> DNA

<213> Homo sapien

<400> 28

accatcaatt gcccggcaag tcagagtatt aacaactatt taaattggta tctgcagaaaa	60
ccagggaaag cccctaacct cctgtatctat gctgcatacc ctttgcataa tgggggtccca	120
tcaagggttca stggcagtga atctgggaca gatttcaact tcaccatcg cagtctgca	180
cctgaagatt ttgcaactta ctactgycaa cagagttaca ctaccccatt cactttcrgm	240
cctggggacca aagtggatgt caaacgaact gtggctgcac catctgttcc tctttcccg	300
ccatctgtatg agcagwtgaa atctggaaact gctctgttg tggctctgtt gataacttc	360
tatcccagag aggc当地aaatg acagtggaaag gtggataacg ccctccaaatc gggtaactcc	420
caggagatgt tcacagagca ggacagcaag gacagcacct acagcctcg cagcaccctg	480
acgctgagca aagcagacta cgagaaaacac aaagtctacg cctgsgaagt caccatcg	540
ggcctgagct cggccgtcac aaagagcttc aacaggggag agtggtagag ggagaagtgc	600
ccccacctgc tcttcaggatc cagcctgacc ccctccatc ctttggcty tgacccttt	660
tccacagggg acctaccctt attggggatcc tccagctcat ctttcaccc tcccccctcc	720
tcctccctgg cttaattat gctaatgttg gaggagaatg aataaataaa gtgaatctt	780
gaaaaaaaaaa aaaaaaaaaaa aa	802

<210> 29
 <211> 620
 <212> DNA
 <213> Homo sapien

<400> 29
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 ctggcttagga gaaaactatca atgctggcag ccagtttcaa tataatgttag aaggagtgac 120
 ttccaaggaa atggctaccc aacttgcctt catgcgcctg ctggccaact atgcctctca 180
 gaacatcacc taccactgca agaacagcat tgcatcacatg gatgaggaga ctggcaacct 240
 gaaaaaggct gtcattctac agggctctaa tgatgttcaa cttgttgctg agggcaacag 300
 caggttcaact tacactgttc ttgttagatgg ctgctctaaa aagacaaaatg aatggggaaa 360
 gacaatcatt gaatacaaaaa caaataagcc atcacgcctg cccttccttg atattgcacc 420
 ttggacatc ggtggtgctg accaggaatt ctttgtggac attggccag tctgtttcaa 480
 ataaaatgaac tcaatctaaa taaaaaaaaga aagaaaatttgg aaaaaactttt ctctttgcca 540
 ttcttccttc ttctttttta actgaaagct gaatccttcc atttcttctg cacatctact 600
 tgcttaaattt gtggggcaaaaa 620

<210> 30
 <211> 644
 <212> DNA
 <213> Homo sapien

<400> 30
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 aaccaccmga cmatttaaca taaaacactt gkcaagctga gtagactgkt ttcttatgkg 120
 aaccacaaaa tattttctct gaaatctaca cttagttaa aaacagagat gggattttg 180
 atattagctt gaaaataagt atatgtatgat gatattaggk gcccactagc acctagttt 240
 tacagctttg cattgkacc ccatcactgc cagggaccca gccccaggca tacacagatg 300
 aaaggacagt ttcaccttct tggaaaaac cttcagaaca attgtcaaca tactctcaaa 360
 tgcctttccc actcagaaaat gaggagcaag gtgtatgact ttagattcaa gaagtataatg 420
 gggctaaata tctttaaaag tataactctg gacaatgtac ttagggacct actacttact 480
 caaaaataggg tagtagcatt aataactaaa tagggcgtga gtcatgagaa agattccctg 540
 catctcttgc caagtattaa cactagttt actaataagc aacggggtag ataactttga 600
 agattgcattc aacttcaaca caaaaaatgt tgaatatccc tcgt 644

<210> 31
 <211> 674
 <212> DNA
 <213> Homo sapien

<400> 31
 ctctctggaaat atgcttagggc agaagtatgt caagtatgtc acatgaagaa aatgtgaaat 60
 tcaagagtaa tccacacgtg agaaactaga caatgtacat tcatgttgc tcttggaaagg 120
 aaagggagag ctgtaaagctt cactctgtcc tacaccggag aaaagcagga ataactttac 180
 cgtggaaata atgttttagct tttatcagag aaaattgtcc ttcttagagca tagagtccca 240
 aaactcaatt ctggtttcc cctgtttttt tttttttttt tttttcccaac atatgtactg 300
 cagcatatca ctttttctt ttgtgcctca gtttccctcag ctgtaaaattt gaaaaatata 360
 tgcattttata atattattaa taataataat ggtaatgttag tactgttttgc taaagcactt 420
 tgagatcctt gggtgaaagg caccatagga gtgccaagta ttattatgtg gccaaggggg 480
 ttatattaaac tgcgttcc caaaggccag gaaagggttgg ggtcattttt cttaaagacg 540
 agctgtaaat atcaacttagg cagccaatag tggactat gaagatgcaaa aactattact 600
 aggmtgataa aatcatagtt tcttaatggc taccataaag gcaaatatca caataataaa 660
 caccataattc cgta 674

<210> 32
<211> 713
<212> DNA
<213> *Homo sapien*

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<220>
<221> misc_feature
<222> (1)...(713)
<223> n = A,T,C or G
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<400> 32

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tattcaactac	akaatccatc	atttttcagc	aggccacagt	ccanccaaat	cctataatat	120
ccttggaaaag	aaactattaa	aaaggataga	catttctgtat	gtaaagtaaaa	cccccaagca	180
acttaatatc	catctgtcag	tcatcaactt	ttccccctaga	ttttttttt	aactagttct	240
gaaagtgtca	agaatagctt	cccttttac	cctacctagg	ttcccccctt	gctggcataa	300
aggccaagca	gtgaaatgaa	ccttgggtt	gagttatggt	aggcaaaaag	aaaaggagaa	360
tttagaaaaat	aaatatgcta	taaacaaggt	acagtagt	gagagttaac	aatcctagga	420
atccctgcctg	tcacaagotc	ccagttccct	gtcattttat	cttcatgatt	agaactgatc	480
ttccatttaa	ctattacaga	aagcagtaac	tattgcaact	atctaatagt	tcacacaaaa	540
gaattaaaaag	cttaaaaata	atttttagga	aacacaatat	tcaaaaatcta	aacacactga	600
taaatttatta	agattaagat	tatwtatgt	ataaaatgaaa	tctcctacc	atccatccag	660
cctttaccag	ggaagaaaaag	caattatcc	atttcagata	qaaatacaaa	aaa	713

<210> 33
<211> 698
<212> DNA
<213> *Homo sapien*

<400> 33

tgcaggggctc	caccggaaaga	gtcaactggaa	ctggaggacc	cgtcttctgg	gtgggggtgtg	60
accaagcgagg	atctggggccc	agtccccatg	tgagagcagc	agaggcggtc	ttcaacatcc	120
tgcgcagcccc	acacagctac	agctttcttg	ctccccatcg	ccccccagccc	ctccccccatc	180
tccccaccctg	tacccatcc	catgagaccc	tggtgcctgg	ctctttcgtc	acccttggac	240
aagacaaaacc	aagtccgaaac	agcagataac	aatgcagcaa	ggccctgtcg	cccaatctcc	300
atctgtcaac	agggggcgtga	ggtcccagga	agtggccaaa	agctagacag	atccccgttc	360
ctgacatcac	agcagcctcc	aacacaaggc	tccaagacct	aggttcatgg	acgagatggg	420
aaggcacagg	gagaagggat	aaccctacac	ccagacccca	ggctggacat	gctgactgtc	480
ctctccctc	cageccttgg	ccttggctt	tctagcctat	ttacctgcag	gctgagccac	540
tctcttcct	ttccccagca	tcactcccc	aggaagagcc	aatgtttcc	accctataatc	600
ctttctgccc	accctctagtt	ccctctgtc	agccaaagcta	gwtatcagct	ttcagggcca	660
tggttcacat	tagaataaaa	ggtagtaatt	agaaaaaaa			698

<210> 34
<211> 605
<212> DNA
<213> *Homo sapien*

<400> 34

aagggtgcat	cattctttag	gaggaagtag	cgtggccgcc	agggtcttgc	gtactccccc	60
cgtttgc	gccaaccctc	cttcacaata	gccacgtcgc	tcatggtgc	cgaggctccc	120
gcgacgtca	cgcgcttc	tcaggctggc	gtccccgag	cccagctggc	ctggccacag	180
cctctgtatgc	accagctgac	aggctgcctc	ctccaggcag	cccctttgc	ttctttgacc	240
caggctgct	cggccttccc	taagcccc	gtgacagatg	gccccgttq	ctctccctgt	300

ccatggtgtt	cctacccatg	gatcctggga	cagggcacag	ggctcctccc	tgctccccag	360
actaggaaag	caaagaaatt	caaacatgag	gaagacagga	ccaggatgca	ggccactggc	420
gcaaacggga	gtccagagcc	ctccagcgca	agccaaaaaa	cctcctggga	gaaaccccaag	480
gccccctccta	aaccacagcg	ccccctgcggg	tctgaatctg	gttcattcat	ttggccaaaca	540
tgtaccgggc	gtctcagggtt	ttgccaggcc	cagtgtctggg	cgctggagac	aaagagccctc	600
gttrcc						605

<210> 35
<211> 753
<212> DNA
<213> *Homo sapien*

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<220>
<221> misc_feature
<222> (1)...(753)
<223> n = A, T, C or G
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<400> 35

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tctgtcccc	tggccacggc	gcccattggca	gagcagagaa	cagaaagtac	ccccatcaca	120
scagtcaaac	agcctgagaa	agtggcagct	accaggcagg	agatcttcca	ggagcagttg	180
gcagcagtgc	cagagtccg	cggtcttggg	ccctcttca	agtcctcgcc	tgagcccggt	240
gccttcacccg	agtcagagac	ggagttatgtc	atccgctgca	ccaaacacac	tttcaccaac	300
cacatggttt	ttcagtttga	ctgcacaaaac	acactcaatg	accagacctt	ggagaatgtc	360
acagtgcaga	tggagccac	tgaggcctat	gaggtgtct	gttacgtgcc	tgccccggagc	420
ctggccctaca	accagccccgg	gacctgtac	acactggtgg	cactgccccaa	agaagacccc	480
acagctgtgg	cctgcacatt	cagctgcatt	atgaagttca	ctgtcaagg	ctgtgatccc	540
accactgggg	agactgtatga	cgaaggctat	gaggatgagt	atgtgctgg	agatctggaa	600
gttactgttag	ctgtatcacat	tcaaaagg	atgaaactga	acttcaagc	agcctgggat	660
gangtagggg	atgaatttga	gaaggaggaa	acgttccac	tgttctaccat	caagacactt	720
gaagaggctg	ggggnaatat	tggaaagtct	tgg			753

<210> 36
<211> 433
<212> DNA
<213> *Homo sapien*

<400> 36

ggggcttgc	atcatttgc	ttgttctgt	tcacaataaa	ggagattcac	ttgggttctgc	60
attttcagg	ttcaatagaa	ctgcttcatt	aaaaaaaataa	tccttagcaa	gcatttcgaat	120
ccttaactgct	ttgatgcact	tgccctcg	cacctgtcat	ttccaaatatg	gtagggtgtca	180
aagtcaaaag	tatttactgg	gagaaaaaaag	agaggagtgg	ttgtagaagt	ctccctaaat	240
cagacatgtc	aagaatcag	ccaaacgtggt	gtatttctca	ttcaatattt	tagtgtgaat	300
tgagacactg	agataaaagac	atcgtgcaga	gataaaatggg	gatacagttt	aatgttagcaa	360
ctcttgagtt	catttttcc	cactgttagca	aaattaatgc	tttcttcttta	ttgaaataaa	420
ttgctcattc	ctc					433

<210> 37
<211> 601
<212> DNA
<213> *Homo sapien*

```
<220>
<221> misc_feature
<222> (1)...(601)
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<223> n = A,T,C or G

<400> 37

aggagtgcggcc	tcaccctgtg	gcaagtacat	ctcctgcggcc	gagtgcctga	60
agttcgaaaaa	ggggcccttt	gggaagaact	gcagcgcggc	gtgtccgggc	120
cgaacaaccc	cgtgaagggc	aggacctgca	aggagagggg	ctcagagggc	180
cctacacgct	ggagcagcag	gacgggatgg	accgctacct	catactatgtg	240
gagagtgtgt	ggcaggcccc	aacatcgccg	ccatcgtegg	gggcaccctg	300
tgctgatcg	cattctctg	ctggatcatct	ggaaggctct	gatccacactg	360
gggagttacag	gcccattttag	aaggagaagc	tcaagtccca	gtggaacaat	420
ttttcaagag	cgccaccacg	acggatcatga	accccaagtt	tgctgagagt	480
tggtgaaaac	aangccgtc	aggacccacc	atgtctgccc	atacgccggc	540
ttggcacact	tttgangatg	taccatttac	caaaatcnn	ganacatggc	600
g				tnaatnanct	601

<210> 38

<211> 713

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(713)

<223> n = A,T,C or G

<400> 38

gcttcggccct	attgattctg	ctcatttata	caataatgag	gagcagggtt	gactggccat	60
ccgaagcaag	attgcagatg	gcaktgtgaa	gagagaagac	atattctaca	cttcaaagct	120
ttggtgcaat	tcccatcgac	cagagtttgt	ccgaccagcc	ttggaaaggt	cactgaaaaaa	180
tettcaattt	gattatgtt	acctctacct	tattcattt	ccagtgtctg	taaagccagg	240
tgaggaagt	atcccaaag	atgaaaatgg	aaaaatacta	tttgacacag	tggatctctg	300
tgcacatgg	gaggccgtgg	agaagtgtaa	agatgcagga	ttggccaagt	ccatcggtt	360
gtccaaacttc	aaccgcaggc	agctggagat	gatcctcaac	aagccagggc	tcaagtacaa	420
gcctgtctgc	aaccagggtt	aatgtcatcc	ttacttcaac	cagagaaaac	tgctggattt	480
ctgcaagtca	aaagacattt	tttgggttgc	ctatagtgct	ctgggatccc	accgagaaga	540
accatgggtg	gaccggaaact	ccccgggtct	cttggaggac	ccagtccttt	gtgccttggc	600
aaaaaaagcac	aagcgaaccc	cageccctgtat	tgcctgcgc	taccactaca	gcgtgggtt	660
gtggtcctgg	ccaagagcta	caatgagcag	cgcatcanac	agaacgtgca	ggg	713

<210> 39

<211> 451

<212> DNA

<213> Homo sapien

<400> 39

aaaaaaactg	actgaaaacgt	tttagatgaa	gaaagttctc	ctcctgtatca	cagccatctt	60
ggcagtggct	gttgggttcc	cagtctctca	agaccaggaa	cgagaaaaaa	gaagtatcag	120
tgcacagcga	tgaattatgt	tcagggtttt	ttgtgtttcc	ttacccatat	ccatttcggc	180
cacttccacc	aattccat	ccaaagattt	catggtttag	acgtaattt	cctattccaa	240
tacctgaatc	tgcccctaca	actccccctt	ctagcgaaaa	gtaaaacaaga	aggaaaaagtc	300
acgataaaacc	tggtcacctg	aaattgaaat	tgagccactt	ccttgaagaa	tcaaaattcc	360
tgttaataaa	agaaaaacaa	atgttaattt	aatagcacac	agcattctct	agtcaatatc	420
tttagtgatc	ttctttaata	aacttggaaag	c			451

<210> 40

<211> 778
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(778)
 <223> n = A,T,C or G

<400> 40

accgcatcct agccgcgcac tcacacaagg caggtgggtg agggaaatcca gagttgcac	60
ggagaaaaatt ccagtgtcag cattcttgct ccttggcc ctctcctaca ctctggccag	120
asataccaca gtcaaacctg gagccaaaaa ggacacaaaag gactctcgac ccaaactgccc	180
ccagaccctc tccagagggtt ggggtgacca actcatctgg actcagacat atgaagaagc	240
tctatataaa tccaagacaa gcaacaaacc cttgtatgatt attcatcact tggatgagtg	300
cccacacagt caagctttaa agaaaagtgtt tgctgaaaaat aaagaaaatcc agaaaattggc	360
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ctatgtgggg aagcattttt ggaacacact ggattanggt tttttttttt aatggttacc	720
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<210> 41
 <211> 696
 <212> DNA
 <213> Homo sapien

<220>
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 <222> (1)...(696)
 <223> n = A,T,C or G

<400> 41

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gcattaaaccc actccctttt acctcacat ggggcaggc cccaaatgttca agactcagt	180
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atatttaagg gaggcaatga accctctccc ccncntcttc cctggccaaa tctgtctcct	300
agaatcttat gtgtgtgtaa taataggcct tcwctgcccc tccagttttt atagacstga	360
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<210> 42
 <211> 509
 <212> DNA
 <213> Homo sapien

<400> 42

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<210> 43	
<211> 388	
<212> DNA	
<213> Homo sapien	
<400> 43	
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<210> 44	
<211> 565	
<212> DNA	
<213> Homo sapien	
<400> 44	
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ctctcgctgt ttggagagaa gggcccttcc cagcacaaag ttgcatttcc ccccccataat	180
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<210> 45	
<211> 661	
<212> DNA	
<213> Homo sapien	
<400> 45	
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gtccccacccctc tggctcttgc agcacaacca acgtgggaaat cacaccctcc agacccctca	180
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<210> 47						
<211> 687						
<212> DNA						
<213> Homo sapien						
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<222> (1) ... (687)						
<223> n = A,T,C or G						
<400> 47						
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<210> 48						
<211> 944						
<212> DNA						
<213> Homo sapien						
<400> 48						
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<210> 49
<211> 449
<212> DNA
<213> *Homo sapien*

<400> 49	ggcacgaggg cttcgaggaa ccagccctga tacctgtgac cctctctgtt cgctaccctc ctgaagtgtc catctccggc tatgtatgaca actggtaacct cggccgtact gatgccaccc tgagctgtga cgtcccgccgc aacccagagc ccacgggcta tgaactggagc acgacacctag gcaccccttccc gacccctccgca gtggcccaagg gctcccaagct ggtcatccac gcagtggaca gtctgttcaa taccacccctt gtcgtcacag tcaccaatgc cgtgggcattt ggccgcgctg agcagggtcat ctttgtccga gaaaccccca ggccctcgcc ccgagatgtt ggcccgcctgg tgtggggggc cgtgggggggg acactgttgg tgctgtgttct tctggctggg gggtccttgg ccttcattttt gtcgtgggggtt agggaggagg	60 120 180 240 300 360 420 449
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<210> 50
<211> 703
<212> DNA
<213> *Homo sapien*

<400> 50	ggcacgaggg tgagccatg cccccccaa ccctgccagc tgagcaaagg acagtttac	60
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<210> 51
<211> 963
<212> DNA
<213> *Homo sapien*

<400> 51
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ggtagctcgca gaagccagga cagtctccac agctccctgat ctatttggct tctaaqcqqq 240

cctccgggggt	ccctgacagg	ttcagtggca	gtggatcagg	cacagattt	acactgagaa	300
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taaagtgawt	tttgmaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaagaaaa	aaaaaaaaaa	960
aaa						963

<210> 52
<211> 628
<212> DNA
<213> *Homo sapien*

<400> 52	60
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cccttaggtat cagccctctt tactgtactc tccggaaatg ttaacctttc tattttcagc	300
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tggccctctc cagggtgttt tccactagtc actactgtct tctccttcta gctaataat	600
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<210> 53
<211> 598
<212> DNA
<213> *Homo sapien*

<400> 53	ctccccccct ttttcccacc ctccacacct cacggggccct gccccagccc ctaagccccg	60
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<210> 54
<211> 592
<212> DNA
<213> *Homo sapien*

<400> 54

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<213>	Homo sapien						
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<222>	(1) ... (504)						
<223>	n = A, T, C or G						
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<211>	749						
<212>	DNA						
<213>	Homo sapien						
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<212>	DNA						

<213> Homo sapien

<400> 57

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ggcctgtgg	gtc	gac	ctgcgggt	ctgcccagg	gt	300	
cccgccccaa	ca	gac	gtctacacga	acctctgca	gttca	caag	360
aaaccatcca	gg	gac	ctgcgggt	gttca	ccac	tg	420
ctgcagg	cc	gac	tgatgc	ccat	cc	at	480
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ttgggctgac	cg	gac	tgatgc	act	ccat	gt	600
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<210> 58

<211> 994

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

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<223> n = A,T,C or G

<400> 58

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agccagaacc	atgccaata	tgtgtctgt	actcaggatc	cg	gatgacataa	300
tatgtgacga	tcaagaatta	gactgcccc	acccaga	ttcatttgg	aatgttgc	360
cagtttgc	acagctcca	actgctt	ctgc	taatgg	ggacctaag	420
gccccaa	aggc	ctt	ctt	ttt	cc	480
caggacaacc	agggtcc	gtt	gtt	ttt	gtt	540
ctggcctca	gaactattt	ccc	ccat	ttt	ccat	600
taggaggact	cg	ccat	ccat	ttt	ccat	660
gtacatctgg	tc	ccat	ccat	ttt	ccat	720
ctggcaagg	ttt	ccat	ccat	ttt	ccat	780
ctgtggaaa	at	ccat	ccat	ttt	ccat	840
gacc	ttt	ccat	ccat	ttt	ccat	900
gaggcttcga	ttt	ccat	ccat	ttt	ccat	960
aaaaggtctt	cc	ccat	ccat	ttt	ccat	994

<210> 59

<211> 639

<212> DNA

<213> Homo sapien

<400> 59

tggtggtgg	ggaggac	ctacttgg	ccc	cc	act	cttgc	60
agatctccac	cttgc	cc	cc	cc	cc	cc	120
cgccat	cc	cc	cc	cc	cc	cc	180
atctcattt	cc	cc	cc	cc	cc	cc	240

ttcttgcac actggggac cacgatggcc gcaccctgc cctgtgggc acggccacct	300
atgacccgt gtcctccacc ccgcctccgg agccggtgca tgggtgtggcc ttcaacccct	360
gggacccgg cgagctcacc tgggtggcc agggcaactgt caccttctgg ctccttcagc	420
agcgtggggc agacatcagc cttcaggtgc gtcgagagcc agtcccagag gcagtgggg	480
ctggagagct gacccgtc tgcacgggg cacctccct gctctattgt ggcaccagct	540
ctggccaggt ctgtgtctgg gacacgctg cggccgctg cttctgtcc tgggaggcgg	600
atgacggtgg cattggctg ttgctgttct cgggttctc	639
<210> 60	
<211> 470	
<212> DNA	
<213> Homo sapien	
<400> 60	
ggcacgaggt ttttattctt tgacacaattg tttcattgtt tgacacttaa tgcactcgtc	60
atttgcatac gacagtagca ttctgaccac acttgtacgc tgtaacctca tctacttctg	120
atgtttttaa aaaatgactt ttaacaagga gagggaaaag aaacccacta aattttgttt	180
tgtttcttg aagaatgtgg caacactgtt ttgtgatttt atttgtcag gtcatgcaca	240
cagtttgcgtt aaaggccgtt aacaagtatt ggggcattt tttttttttt tccacaaggc	300
attctctaaa gctatgtgaa atttctctg cacctctgta cagagaatac acctgcctt	360
gtatatcctt tttcccttc ccctcccttc cagttgtact tctactaaaat tttgtctt	420
tttttttattt tttaaataaaa ctgacaaaatg aaaaaaaaaa aaaaaaaaaa	470
<210> 61	
<211> 535	
<212> DNA	
<213> Homo sapien	
<400> 61	
ggcacgaggg gttcttggc caatttcttg ctgactcgtc cccactctgt gtcggaggtct	60
ccggggaaaga cggtaaccat ctctgtcaco ggcaacagag gcagcattgc cgccaaactat	120
gtgcagtggt accagcagcg cccgggcagt gccccccacca ctgtgatcta tgaagataac	180
caaagaccct ctggggtccc tgcacgggtt tctggctcca tgcacgttc ctccaaactca	240
gcctccctca ctatctctgg actgaaggctt gaggacgagg ctgactacta ctgtcgtct	300
tatgagagca gcaatcattt ggtgttcggc ggagggacca agctgaccgt cctaggtcag	360
cccaaggctg cccccctcggtt cactctgtt ccacccctctt ctgaggagct tcaagccaa	420
aaggccacac tgggtgtctt cataagtgtac ttctacccgg gagccgtgac agtggccctgg	480
aaggcagata gcagccccgtt caaggcggga gtggagacca ccacacccttc caaac	535
<210> 62	
<211> 696	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(696)	
<223> n = A,T,C or G	
<400> 62	
ggcagtatcc aatggggaaat cagctctaaa aggaaccaga ccaacgtttt ccagcccttt	60
cattntgggtt actgagggggaa gggaaagaatg ggagggggta ttcttgcata gtggatggaa	120
aggaaacaca ctgtcaaattt acttatatctc cttggtttttca tattacagta gaattctcca	180
ccatattttt tattgtctat gggggaaatggt ggagatgtgtt accttgatttta gaagtgtctg	240
gagggggata aatgggggggata aatggaggattca gttggtttttca gaaaatgttta aagtctttaaa	300

ataatgcgtc catctgaaga atttttcta aaaccagagt ttataaaaat atcaactgata	360
cagcctgccc cctcatttcc ctgccacagg agatgtctt gactagagac acttgtttaa	420
taatagctt tctctgatat tcccaagtgc ttccctctgt gtgaggaaaag gatagaaaatg	480
ttcaggacat catcatacag gtccttcato tacaaagttc cagtagcagt gacgcctaca	540
cggaagactt ggaactgcaa acaggctggg gtcacccatg tgacatctga cgctgtccaa	600
ccagaagttt gatttttgtt ctgggggtga aggagggaaac agacgtgtac taaaggacta	660
aaataatgg tctatacataa aaaaaaaaaa aaaaaaa	696

<210> 63
 <211> 256
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(256)
 <223> n = A,T,C or G

<400> 63	
taatattttat tgaagncccta ctttgcctc tacatagggt agcttctgtc agggaaatgtt	60
ggttcttccc aagaaacact gattttcttt cagggagact tcattgtgttc attttttcc	120
accacacgca attttaagaa attataatat gtaatatttg atatctataa agagtanatc	180
taacgtgaat aaattatgaa gcataactaat gagtacccat gacccatnac acatatacat	240
taaaacattt taaaata	256

<210> 64
 <211> 678
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(678)
 <223> n = A,T,C or G

<400> 64	
ggcacgaggg ctanaagcca tcgcattttt ctccgtattc aacaagccca ttataacaag	60
tctttcacgc tcaaccattc aaacaatccc aacaatccc gcctaagaat ttccctggcat	120
tttgcataaa tggctgtggg ttttgcatac tttaagctcc ctggaaagca ggatataagc	180
ccaggctgg caggctttt ctgcatacct gctcttgcac atagagtttgc cctcatgttt	240
gcaagaaggc tgccatagct ccagatggca catagacatt ccaggcagca ggaaaaagga	300
aggagcactt aaccgaagga ggtcaggag ttggttagtc tccacctgaa gaagagagcc	360
atgaaccaggc ttcaatgtgc taacgggctc ctgtgagtgc atctttggac ttttctggag	420
gttgcataatct agatgtggta tggatctttaa agcagccacc aactcctccc attaccttcc	480
aagtgcggcc aactacacga tggagccctc tccctgcctc tggatctggg ctgagccctc	540
gacttgcgtt gaccaacaga atgcagtgaa agtgcgtccg atactaccct ccctgcctca	600
gacttgggat acctgcagct atattcttcc attcctcagg acttgaaaa acgggtctca	660
ncatgcctt ccagagcc	678

<210> 65
 <211> 678
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(678)
 <223> n = A,T,C or G

<400> 65

ggcacgagga ggacacactc	aggatagaaa ctttatgtgt	atagggaatg tggcacagcc	60
tttagccagg agtcatactt	catcagacac cagaggacac	acacagtgcgt gtggctttt	120
cagccattgc tagataccaa	agtggagaca ttctgtgtgt	gattatgcatt gagactgtac	180
tggtaagact tgtatctcca	tccacctgaa ggagaattgc	tggctcattt tcaggagccc	240
tgccttcctt cactgtggat	ggtgggttgt ggaaacccgg	tcaggtaatg atagtggcag	300
gagggcagtca aatgccagg	cagatagggg tgggtacctg	gtgaaacccca accttaaagc	360
tgaagacagt cccggctaaa	tcctcatactt gaattgagaa	cctgtcttcc catttggtgt	420
gccttcctcc gattgatccc	aacccttcac ctattttacg	tatacctgcc ctttcctaat	480
tggtttttac actgctgtgc	ccacccctttt agtggtgctt	ttgcatactt acaaatacgt	540
caacgtgtat tcccctattc	tgagccctata aaagacccan	actcagctgc agtgaggaga	600
gaaatccccct gctgnggggg	gtggggacca ctccctgcat	ccctctncac tganagctgt	660
ctttttgctc aataaaat			678

<210> 66
 <211> 606
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(606)
 <223> n = A,T,C or G

<400> 66

gcatacaactg ccgccagccc ttcatntnt	ccgccttttc ctagacgtgc	tacaccctgg	60
tgagttctac ctggaggaag ggatcaactga	tgaagaagcc atctccctca	tcgacccctgga	120
ggtgctgaga cccaaaggccc atgacagaca	gctagagatt gcaaaacaaca	gctcccccagat	180
tctgcggcta gtggagacca aggactccat	cgagatggag gaccgttca	cagctaagct	240
gagcttttag caagggtggct cagagttcgt	gccagtggtg gtgagccggc	tggtgctgcg	300
ctccatgagc cgccggatg tcctcatcaa	gcgatggccc ccacccctga	ggtggcaata	360
ctcccgctca ctgctgcctg acgcctccat	taccatgtgc ccctccctgt	tccagatgttt	420
ccattntgag gactatgagt tgctgggtgt	tcagcatggc tgctgcccct	actgcccgcag	480
gtgcaaggat gaccctggcc catgaccagc	atccctggga cggcctgcac	cctctgcccgg	540
ccttggggtc tgctgggctg tgaaggagaa	taaagagtta aactgtcaaa	aaaaaaaaaaa	600
aaaaaaaa			606

<210> 67
 <211> 579
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(579)
 <223> n = A,T,C or G

<400> 67

ggcacnaggc ccaatttatat	gttcattttt tatattttt	ggtcggggaa aaaattgacc	60
tgcagtanaa aaaccccttga	ccatttttat gtccatttga	tactttccctt ttatcatct	120
taaaaaaaaaga taacttagtac	taatcattgt agtggctaa	gtgtgattta actcttgaag	180

tcacaccctc	cgaaagatga	gtagaaacca	gcaccagcac	agcccagatc	ttctcttcc	240
tctccttttc	ctcatttatt	cctaaaggaa	tctgaccatt	ttacgtctct	acggcccaaa	300
aaaagacaaa	aataaaaatt	cctttttatt	cctgtcaact	ggatggaaac	acaaatttca	360
tggagctgt	taccatcgaa	gaaacctggt	gtctggcatg	aaattactgt	aaagaacttc	420
ctgtaaaaca	cgttcttaa	caaactgaaa	tgaaaagcat	tggagcgtct	gaatgaaga	480
cgtgacctcc	tgctggact	ctgatggtct	ttagcattca	ccttcgtgt	tcttcagtgt	540
ctcattgtca	tccctgcttc	tgtttggtct	tagagtgtt			579

<210> 68

<211> 258

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(258)

<223> n = A,T,C or G

<400> 68

ggcatntggc	cctgaccana	tccttaaccc	tagcgatggc	ttgggagatg	ggggggttgg	60
tagcattntc	tttcttggcc	cttccttatac	ctaggaaaan	atggttcetc	tccttgcgtg	120
tgtctcttcc	ccccacccct	aattcttctg	ctctgttgg	gaagacgtgg	aggaaaaggt	180
gacttctgccc	cccacccgtc	ttaccccccac	tgtantggcc	tttggagatg	cccccaccc	240
ccccccacca	actctcgc					258

<210> 69

<211> 628

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(628)

<223> n = A,T,C or G

<400> 69

ggcacnagga	gaatntttg	gaataaaaact	gactgataaa	actggaaatg	ttgctcgggc	60
tgttaactgg	cagggaaagat	ttcagcatct	gaatgagtc	cngcacaact	attnaagaat	120
cactcgtatt	cttaaaagcc	ttggtgagct	tggatatgaa	agttttaaat	tcctcttgt	180
aaaattttt	cttcataaag	ctcttgcgtt	gaataactatt	cccaatattt	agcagagtgc	240
tctagatgt	tttgcgttata	caatttagaga	cagaagagaa	aggagaaagc	tcctgcgtt	300
cgtccccagaaa	cactacacgc	cttcagagaa	ctttatctgg	ggaccgcctc	gaaaagaaca	360
gtcggaggaa	agcaaaagccc	agaaaatgtc	ttccctctc	gcctccagtc	ataacagtca	420
aacttctatg	cacaaaaaaag	ccaggactc	caaaaatcc	tcctcagctg	ttcattttaaa	480
tagcaaaaaca	gctgaagaca	aaaaagtggc	acccaaaagag	cctgtggaaag	agacagacag	540
gcccacccan	agcccagcaa	tgaagctgcc	aagccaaagaa	atacagaaga	aggacagataa	600
tgctganaac	atgaattctc	aacctgag				628

<210> 70

<211> 439

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (439)

<223> n = A,T,C or G

<400> 70

ggcacgaggc	gcacacccgc	tggcgcccc	ctgtggagac	cctggaaaac	atcatgcaca	60
ctgttagacac	gaggctgcct	gagttctca	agctgcaggg	ctgtttccgg	gaggagctca	120
tggaggcctt	gcacctgcac	ctggtaagg	agtacatcat	ccaaactcagc	aaggggcgcc	180
tggtcctcaa	gacggccgag	cagcagcagc	agctggctgg	gtacatcctg	gccaatgtcg	240
acaccatcca	gcacttctgc	accagcagc	gctccccggc	gacctggctg	cagcctgctc	300
tccctacgt	ggccgagatc	attgcctgc	aggaccccag	tgcctcaag	attgaggtgg	360
ccacttatgc	cacctgctac	cctgacttca	gcaaaggcca	cctgancgt	atcctggcca	420
tcaaggggaa	cctatccaa					439

<210> 71

<211> 328

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (328)

<223> n = A,T,C or G

<400> 71

tnggaactca	ggtttacnca	aactgagggg	gccccagccc	tngtaccncc	cctgttaccc	60
caggatccat	ntgcccctcan	aaaagngttc	aggtacagca	gctgaggctg	ccctgaggaa	120
tcaagggggc	attaccaagg	ggcaggaaaa	ggatatgtaa	nagngggct	tcatggtana	180
gcttgaccca	anaactactc	cnctatnnga	tggcccaagac	tgactccatc	ccctgacttt	240
ccctttgact	tcnccctgtt	tgtaaataaa	acaataaaaat	ggaaggtgct	gtggacggga	300
aaaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa			328

<210> 72

<211> 721

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (721)

<223> n = A,T,C or G

<400> 72

ggtttctgtt	gctattctgc	caagttatcg	agctcctcct	catgtttcaa	cattccatct	60
tcccggttct	atcctcgact	ccaaagtaag	ccttcttagc	tccaaatcagg	gatgaggggc	120
tcaacccctt	ctgtcctcaa	agaggccaaa	cgcagtgcac	cagtcggtag	ccttcacttt	180
tagatgtctt	attcatgtaa	aaaagaaggt	gccccccacca	ggcttacatc	agcaataaagc	240
aattctaattg	caacgatggt	gtccacattt	taccccaatg	tgtgcccattg	tatgcctttg	300
tgcggctgtt	attattgtt	gcgccttctt	cacttagagg	ggtgatgata	aactgtggcc	360
accttgattt	caacccacat	ttctcttttt	ggggagcttc	caagtaacag	gccatatttt	420
acctccctcc	aggaacagt	ggcactgcac	accacccctgt	gtctgctcat	aggatgacgc	480
tggagatccc	cacacttact	ctacccttctt	ggcaaattgg	cattccggtg	gtggtttttg	540
tttcctttaa	cacattaaat	aaatgagtat	ataggatgtg	aggggaggggg	tgagaacaac	600
tagctgttgt	atgtgttgtt	tatataacttt	accatccgac	ttctttnctt	tttttttttt	660
aaaaaaaaaaa	aagtgttgta	ctgggttcaa	gtttcatcat	aaaaaaaaaa	aaaaaaaaaa	720
a						721

<210> 73
 <211> 596
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(596)
 <223> n = A,T,C or G

<400> 73

attgtacaga acagcccagg tagggaggac agntgcucca ggtcccatag gantgcacgc	60
ctcaagccca cgtcatgcag agccactca gtcacccctgn tcagggcacg tggtttacct	120
gcattccctt nttcaggcct ctacgtgtgg aggacgttacc atntgacctn tgcaggagag	180
aaactcacgg aagacagaaa gaagctccga gactacggca tccggaaatcg anacgagggt	240
tccttcatca aaaagcttag gcaaaaatgtga gcctccagac aggacaaccc tnttcatcac	300
tggtggtgtga gcttttccc agcaggaatg ggtcctcgaa tcatcgcc tnttcacan	360
aaggacgtt gtggtggcct caccggcctt atgcccaca gtaactgtca gcataaaacct	420
ggggggccctc aggacttagga cagggtgagc cagtgcctcc tccttcatg tacttggcct	480
gagactgacc tctccctagg tccaaatgcc ctatcgccat ggcagaccca cggccctggcc	540
cactgtataa aataaacctg tttgctntt agttgaaaaa aaaaaaaaaa aaaaaaa	596

<210> 74
 <211> 302
 <212> DNA
 <213> Homo sapien

<400> 74

ggcacgaggc ttaaaccaag tttctctgca gctcttcgg ttctgtttac agtgtgtggg	60
aaatctgatt tttttccctt agtaatagtt tgataagaaa tttagtgtat tgactgcctc	120
agtacacaaa ttatcttta aaggtgtggg agctggggg gacccaaatgt tacctgttt	180
tttgctgttg attgctattt tcagaagccaa accatgtttt tcacttacag taggagtcaa	240
caaattttggg atttttagaa ggggaggagg gagctatgg tgaagactg ctgtcatatt	300
tg	302

<210> 75
 <211> 635
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(635)
 <223> n = A,T,C or G

<400> 75

ggcacgaggc ttaatgtgac ttccctgagt taacactgaa tagtatttct aaaatttttt	60
gtactttattt ttttaatgtta acttgttcta tctatctata tatatatttg atagtttg	120
gaataatatac cccccaggattt ttccatattta aatgcttaattt atcttttgc ttcttttca	180
taagcagatc tggcatttt tacagggctg ccgcattaaaga gaactcattta taatgaacgt	240
tttattatattt ttgcaggatcc atgcctgttg tccattgtt gacatgagca cccctgtttt	300
ctctggagaa atacctcccc tctctggggt gttccctgtg gtatgttctt tcaggtatcc	360
gttccacttag ctacagggtga gcattttacc cattgttggaa taatggtaat ctcttttca	420
gaatttttagt tctgttaatttcc atttgtacat gaaccagaaa atgtggaaac tcatttcc	480

ttgtcccaga attctgttga gaacatccat tcattctggc taattgatta caagaataac	540
tgnngatacg atccctttan aacctgcttc tctgatctgn gtgtttcctc acttctcaat	600
aaaaatgtct tttgctaaaa aaaaaaaaaa aaaaa	635
<210> 76	
<211> 678	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1) ... (678)	
<223> n = A,T,C or G	
<400> 76	
ggcacgaggg tcttgattct tggcttgccct ctccctccaaat tccaaactta gtgaaatggc	60
cttaagcatt ttaaaactgtt tgatatacatt agcgcattca tgcccttctta aacgcatttc	120
aaatgtcaac caggaaggca caccactgtt ttagttttat actgcccgtg taaaatttac	180
cacaaactta gtgacttaac acaaatttat tgcaattctg taggctggaa gtctgactat	240
gggtctcact ggactagaat caaggctggc aggctgcctt ctttccttggaa gtttcttaggg	300
gagactctgt ctccctgtcc ttccaggctgc tggcagaatc cacatccctt cggtggcagg	360
gccaaggctcc ccactttctt getgactgtt aactaaggcc acttccagct tgttagaggct	420
gcctacattt cttggctctt ggccccctcc tccatcttca gagctagcag gttcagtcgt	480
tgtcacgaac catttctctg gtccctgtca gacagggaaag gttgtcccta aggactcatg	540
agatttaggtt gggcccagcc agataataca tgataatctc cctccctcaag gnttttaata	600
ttaaacacat ctgcaggaca cattttgcca tgtaactaac attcaactggt ccaggggatt	660
aaggaatgaa ccctctt	678
<210> 77	
<211> 669	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1) ... (669)	
<223> n = A,T,C or G	
<400> 77	
ggcacgaggg agaatcttaa aaaaaaaaaa acgtttctca ctgtcttaaa tagaattttt	60
aaatagtata tattcagtgg cattttggag aacaaagtta atttacttcg acttcttaaa	120
ttttttaaaa agactataag ttttagacatc ttcttcattt aaatttaaag atatcttct	180
cctcttgcattt aatctatcaa tattgataga agtcacacta gtatataccat tttaaatcat	240
tttacactttc ttatttaaga agatattgaa tgcaaaataaa ttgacatata gaactttaca	300
aacatatgttcc caaggactctt aaatttggatc tcttccacat gtacaatctc atcatcttgc	360
agcctataat gaagaaaaag atctagaaac tgagttgtgg agctgactctt aatcaaatgt	420
gatgatttggatc attagaccat ttggccctttg aactttccata ggaaaaatgaa cccaaacattt	480
cttagcatgtt gctaccatc ctctagaagc tgggatggac ttactattct tggtttatatt	540
ttanatactgtt aanggnctt tgcttctgtt attattccaa gactggagat aggccaggctt	600
aaaaaggat tatttttc cttaatgtt ggggctaaaa ttcttcctt aaaaattccctt	660
aaaaataagg	669
<210> 78	
<211> 134	
<212> DNA	

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(134)

<223> n = A,T,C or G

<400> 78

ggcacgaggg gtcgattta atagcgaatc cttttcttg tagaggtaag taaaatttc	60
ctgacaagg tgcctctnt tcacggcaca gacaatggc ggnctgttta tgaggggtga	120
gaagngacnc ccgc	134

<210> 79

<211> 396

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(396)

<223> n = A,T,C or G

<400> 79

tanatgcaag tntnttgtna gatatacgta ttgagatatt acncctagtc tggcttgc	60
ctgttttctt tatgtctttt gatgaatana agtttaat tttgacaagg tcaaatttat	120
ttttttcttt tgtttgatat ttttntctc caatthaacc ccaagatttc anatattntg	180
ctcttattana taaactttat atttttatat ttgtgatctn ctttgaattt atatgtatgt	240
tgtgaattat ggatcagggt tnttttttcc ccccatacaa gtaeccagtc attgtacnc	300
tgtttattga aanaatttac ctccctcat taaatnct tgccaattag taaaaatca	360
attaccata aaaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaa	396

<210> 80

<211> 731

<212> DNA

<213> Homo sapien

<400> 80

tctacatcat cctgagagcg cttttagact ggacagaact gtaggaactg ccgtcttta	60
tggtagatgt gccccatcac aatatacctg caggtaaaa ctctggacac ggcttattgc	120
agctggagga gtccagggtt aacatgtgga ctggaaagaa gaagccgtcg ggggtgaggt	180
acaggcggtt catttgtac agcccgtecc gatccaccag cagggtcacc agccggatgc	240
ccgcggccca cacttccaca tcgtcacga tcccggttac cgccaaattcg ctctcgacaga	300
acgcctcgcg ttctgtccaga tggaccggc aggcgcgcgc gcagggtca ggcggggct	360
ccgcgtccct ctgcggcggtt ctgaggccga agctgaggct gaagccgcggc ggcggcgccgg	420
gcgcgggtcc cggggccacgc gggccggcgc gggccgggtt ggggtggggc tggccggccgg	480
agecccteggt ggcgagcgcg gggggccggg cggccgggaa gcgcaggggcc cgtgagcgcg	540
cgegtcgccgg ggcgtctcc gacgcgggtt cggccggcg cgaacgcggc ttctcggtt	600
gcgcaggcg cggccggcc gggccagcgg gcgcgggtgc ggcctcccccgg aagctggcct	660
ggttgcggc cggccgggtgg ggttccggc ggccgggttc aggccaggcg cggacggcg	720
gagcgaccc g	731

<210> 81

<211> 396

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(396)

<223> n = A,T,C or G

<400> 81

cccttcatcc caatccntga	gaagttcttt ttctgttcc	tgcccaacat natcaacagg	60
accttattcc catttcctg	ntcttncntn anccagntat	tggnnngnggt tttgaaatgg	120
ctnatnatga ggaanagtnt	gatccnacac ttggagganc	naggggtgca ggtggtnnn	180
tggtgcctta atgaanagtc	ggattttga gca	gcgtgggagc cacnggcgtc	240
ataacggatt atccnnnagc	cctnnggcan tacctggaca	accatggncc agctgcccgg	300
accttcaag tccagaancc	tngaggtntc ctgttntnt	tccatgaaaa ataaatattt	360
gccttcgat caaaaaaaaaa	aaaaaaaaaa aaaaaaaaaa	aaaaaaaaaa	396

<210> 82

<211> 502

<212> DNA

<213> Homo sapien

<400> 82

ctcagaggaa agaagaaaaag	ggccaggagt cagacgtcac	acccgggggc tccccttcc	60
catgtagaag tggtgcatg	cgtcagtctc ctttacagag	gggtggatgt atccgtggag	120
gagggggcctt ctctctttct	aattgcacta tacttgtct	agcttcagtc tggagatact	180
taagacctcc atgggtcgt	gatccataga cttagcaagt	cttgccttat ctatggagct	240
cgatggtgag aattgtgacc	attgtctgat gtccatagtt	ccttccccct agattgttcc	300
tttccacgga ttgtgttcat	ctgaaccatt ttattttta	tttacccaaag tactgtactt	360
gctatattgc agtgtttca	aaacccaaatg tttctttttt	tgtgttttta atcttcgata	420
cttggtgcaa tagaagctgc	aaagatgtgc cacttatct	atgaaatgga gttttgtata	480
ccaataaatt ctagttaaa aa			502

<210> 83

<211> 666

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(666)

<223> n = A,T,C or G

<400> 83

gatttttggat ttgttactt	atttatgaac ttacttgag	acagaatatg gttaaaattt	60
ggaacatcta ctttgaatga	gttttatttt tctattttga	atttgcctta tttatattca	120
aaggctttagt gaaatactgt	aaaggaacat tagaaaaagg	acaaataggc tataaccatc	180
tatcttaaaa tcagaccctt	agtataagca cctcttttc	tttcccttt tgacaatttta	240
gtctcttatt taggtccatg	taatttattt cattccatta	ttttttatgt gtttatttctt	300
aaaaacaaaaa atttttagcc	actcccattt atttccat	gacatggtcc tataatgcag	360
tacttaacac agtgccttgc	acatagttagg cattcgtaa	atacttacat gcatgaatga	420
ataatgtatt ttcagtgtaa	caaattttt ataaaaagtgt	agttcgactc ttcttggct	480
tggagtttga gactacagaa	ttacaggaa tgaagagagg	tataagttaga tattttatgt	540
gaaaatgaagt ataaattaat	aacttgactt acccctccat	aagttactgc taactggaga	600
tacccttgc tgcccaaccc	gtaaaggaaa aagntctatt	tctatatttta taggacattc	660
ttctca			666

<210> 84
 <211> 199
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(199)
 <223> n = A,T,C or G

<400> 84
 aanntactta agtattcaa agaatgttat ctttcttgc aagtaattt aagcacatgg 60
 gaaagattct agactttttg tttcttgc aa canacagtgc cctctgtgc tagaaacatt 120
 tttctactta ctatcattt tattgtggct tgagctcanc tcaatctggc gcagatgacg 180
 ctggacaact actaaccaa 199

<210> 85
 <211> 670
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(670)
 <223> n = A,T,C or G

<400> 85
 cacttcagga gagaacttca tagcacaatg tctttctata agatattttt aatgatttag 60
 tattttacaa catttggta ccatatttt atataccatt ttttctatc tgcccagttt 120
 tattaaaaaa actatatattt attttctaaa gaaacaatca tattttata caaaattatg 180
 ttttcaggta acgaaataga tgggggtac agtggAACAT aagcagtgtt acccctggct 240
 gggagtcaatttatacaac aaatgggtgag ctggAACATG ccctgtctgt gctgtccctc 300
 ctgtgtctggc tcgcggatgt gtggcaaca ttgccttatac acgctagggtt cacctgacac 360
 tttaaaagga aaaaaagttc catagagttc tgggtcaca aaattgtttt gcttttatca 420
 aataactttaa tagaaccaaa gttgcagata ttggaaatgtt tggaagtatc tcagtctctg 480
 cataagagga ttaaagtatg aaaggatcat ttaatgactg ttttacttat aagtcataa 540
 gtaatccacc atttctttagt gatgtatgtt aaggctgggt aggtttgtac tctaaggagc 600
 ccagatcata atgcagangca ttcccttanc ccttagagtt tcttgcacaa atttaaaaaa 660
 agacntattt 670

<210> 86
 <211> 401
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(401)
 <223> n = A,T,C or G

<400> 86
 atttccccac gagttggatt ctggccttca gagaccagga gggagtgtct gggccgcang 60
 tggcactg tggtagagt gtgtgtctttt gcacacacag tgcagcggga acgggtgggc 120
 tggctgggtgc tgaagacaga cacactcctg agccaagggtc ttgtcttcaa cctccccgtc 180
 ccgttgtccc attttgtctt gtgaagggtgc aaatccctttt cttcccttcc catctcaggc 240

tctcctgttt	tccctcaggg	tccagtatgc	ctttgagctt	tagctgttaa	aaaggaaccc	300
ccgtgacttg	acacagctt	cacanctggc	tgctangacc	ggcgggctgg	gtgttacgt	360
gtgtctgtgt	catggatgca	atgcangccc	tnangactg	t		401
<210> 87						
<211> 373						
<212> DNA						
<213> Homo sapien						
<220>						
<221> misc_feature						
<222> (1)...(373)						
<223> n = A,T,C or G						
<400> 87						
cttttttttt	ctttttttta	tttgaaaact	actttancaa	taattaattc	catgattatc	60
acattctgcc	attaaggat	attagtaccg	taatactgaa	gaaattttat	taagtctgaa	120
cttcgggggt	aggcagcttc	tttgcgttctt	ttctatccac	cctgtcggt	tgaggtat	180
gtttcttgc	taataaacc	tttgataactt	taaccagaaa	tcagctata	aagctat	240
tgagtatagt	tnnnnnnnnn	aaaaaaagg	aacttgggna	ataccttcca	nnctgaccc	300
cntntaccaa	gatattttc	aggcgttta	tttactatgc	nctaacta	tgcnctttt	360
ctgaaaatatt	ttn					373
<210> 88						
<211> 507						
<212> DNA						
<213> Homo sapien						
<220>						
<221> misc_feature						
<222> (1)...(507)						
<223> n = A,T,C or G						
<400> 88						
ccaggaggcag	cccattcc	atgc	agagactc	gcaggcagcc	aggccacang	60
acccttgtgg	tcccacccca	cacacgccc	attcttcc	gaggctggc	tcccttccca	120
cctctctcac	tccttggaaaa	cactgttctc	tgc	gac	ttcaccttgc	180
tccccacccgc	agacaggacc	aggattcc	atgatgtt	ccatgagtc	cctgtttgtt	240
tctgaaaggg	acgctaccc	ggaaagggg	tggacatgg	gaaaggggaa	gtttaggca	300
taaagtctagg	ggttccctt	tttggctgt	gaaggctcg	gcatgcctgg	atggggctgc	360
accggctggc	ctggccctc	agggtccctg	gtggcagtc	acetctcc	tggattgtcc	420
ccgacccttgc	ccgtctac	gagggccctc	ttatggctg	ggttctaccc	aggtgttagg	480
aacactcttgc	cacagatggg	tgcttgg				507
<210> 89						
<211> 796						
<212> DNA						
<213> Homo sapien						
<220>						
<221> misc_feature						
<222> (1)...(796)						
<223> n = A,T,C or G						
<400> 89						

gactttaatg ggnatatggg ctctacactc atagggaccc acatgttcca agcctccagc	60
tgtgtgttct gcttcctcaa gcagcagctg actctgatat tccccatctc accttagcag	120
tctatatacaa gcaaaggcga tgagaatcc catgcaccca tcataatgt aataaaaggc	180
agatattatg tggctcttgg aaccagtctt aggcatggag gttgaggatc aggagtact	240
tgagggtaact gactggcaga gcaggagccc cgttatgg gacaaacaccc gccactttaa	300
gtttagtctt catttttagc cttctggatt taaggaaatt acttttttaa aaactataag	360
cagccaaaaaa aagcagacag taaaatgcag ataaaacagc tcgggcacag aggaagggtgg	420
aggaaaaagtc tcttggtaa ctgccaaact tcaccctcat acaatgggccc ccagtaaaac	480
agtgggcctt aataagcaca ttcccttccc tccaggtgca ctaaaatagg gaagctaaaa	540
gcagacttgg ggggtatgcc tacagctgca gaaaaatgtt aaaaagcaaa cacaccactc	600
tcctcccat ataagcaca caaaaaaaaaa cagaagcagt ccaagctnt aagaaactct	660
ccaccctaa atccttaaac actcttagtc tgttagaaaag actctaaccct aattcagcca	720
gcagcccttc tcaggtgtgt tttntntaaa ataaacctgt nttaaccatc aagccaaaaaa	780
aaaaaaaaaaaa aaaaaaaaaa	796
<210> 90	
<211> 462	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(462)	
<223> n = A,T,C or G	
<400> 90	
tagaacatnc tgaatttttt ttgtactgnt ggactntatt cagtgtcatg tcctataatct	60
gatcaagttt tcaagnagat aattttanaa tggaaaaagaa aatccctttt tngggaaacaa	120
aagacgtttt atatgtcag tatgacaaaan aggagtttca nagacaactt tgaatccttg	180
tcagcctggg gaccagcncc agaggaatnn ccaaggccaa ctcccatata tttgcttccc	240
ccaaattgct gcccctacag actcaaaagct cttttttttt gttttgtgt ttntctaaaa	300
atttactgtt ntttgtcgat gctatataag ccagggagtt ttaagacgcc agctnttga	360
natttgnntca ttccctgtta ttcccccacat anatattaca tatacccgng taataaattt	420
atgtttgtta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa	462
<210> 91	
<211> 591	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(591)	
<223> n = A,T,C or G	
<400> 91	
cgggccttgg aaggcttga cctggatctt gcacagtggg gagtcaatgt ccagccctac	60
tccgggtccc cagccaaacctt ggccgtctac acagcccttc tgcaaccctca cgaccggatc	120
atggggctgg acctgccccga tggggccat ctcacccacg gctacatgtc tgacgtcaag	180
cgatatacttccat ccaacgttccat cttcttcgag tctatgcctt ataagctcaa ccccaaaaact	240
ggcctcatttgg actacaacca gctggactg actgctcgac ttttccggcc acggctcatc	300
atagctggca ccagccctta tgctcgeetc attgactacg cccgcatgag agaggtgtgt	360
gatgaagtca aagcacacccctt gctggcagac atggcccaca tcagtgccctt ggtggctgcc	420
aaggtgatcc cctcgccctt caagcacgca gacatcgta ccaccactac tcacaagact	480
tttcgagggg ccaggtcagg gtcatcttc taccggaaag gggngaaaggc tggacccccc	540

aagactggcc	gggagatccc	ttacacat	ttt gaggaccgaa	tcaacttgc	c	591		
<210> 92								
<211> 647								
<212> DNA								
<213> Homo sapien								
<220>								
<221> misc_feature								
<222> (1)...(647)								
<223> n = A,T,C or G								
<400> 92								
gaataactag	aaatttattt	gatcagg	ttt cacatttgc	tttttga	aaaaa	ctactac	aa	60
aaagatttca	ccaatttaca	actccatcat	tagtaagaat	gcctgtttgc	ctatagtc	tg	120	
ccaaccctga	atcctt	aaaaa	attttgc	atctggtagg	caaaatttct	ttcttttctt	180	
tgaatattaa	tgaggaggaa	catctttca	tg	tttcttgg	ccat	ttccttattat	240	
gaattgctt	tgcccattt	ccttttttta	attatgaaag	tctaatgact	accttctcat	300		
tgtataaaaa	acacagt	ttct	ttgaatagag	agacc	ctccaatgct	accaatcaca	360	
ttccacttac	cacagttaa	catacatc	ctagtcac	ttccgtac	atatacatac	420		
acataaaaaac	acttttaca	taaataggat	ctcatattct	gtagctttt	aaaatttgg	480		
nctcaaaaaaa	aganaacang	gctttaattt	tcttaatgg	gtgaatatga	ataaaacta	540		
tgaaaatg	cc	ttt	tttctctc	gtattacat	tgccaaagna	600		
aacatcctat	tcanatgt	tt	gngcatgt	gn	gngnaat	647		
<210> 93								
<211> 740								
<212> DNA								
<213> Homo sapien								
<220>								
<221> misc_feature								
<222> (1)...(740)								
<223> n = A,T,C or G								
<400> 93								
gtcatgatag	aggaaat	aa	tgcaaggaaa	aaaaacaagc	ccagttgg	tggcttg	60	
tactgcaagg	ctttacaatc	agattat	atc	acatacatag	atgaaact	cct	120	
aatgc	aaac	tttgc	tttgc	gac	cttgc	at	180	
ttcttggcc	catg	cttgc	atacc	cg	cttgc	at	240	
gccagaaaatg	ccat	catg	ccag	cg	acat	ca	300	
gtacaagagt	ctccat	cttgc	tttgc	tttgc	tcttgc	tcttgc	360	
cttgc	tttgc	tttgc	tttgc	tttgc	tcttgc	tcttgc	420	
gagttagatt	acaat	gtc	tttgc	tttgc	tttgc	tttgc	480	
ctgtatttca	atag	tttgc	tttgc	tttgc	tttgc	tttgc	540	
gg	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	600	
tgtgcatttgc	aa	tttgc	tttgc	tttgc	tttgc	tttgc	660	
tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	720	
accccttact	tcacaat	tttgc	tttgc	tttgc	tttgc	tttgc	740	
<210> 94								
<211> 608								
<212> DNA								
<213> Homo sapien								

<220>
 <221> misc_feature
 <222> (1)...(608)
 <223> n = A,T,C or G

<400> 94

ttttacaatc	ctaggaaggc	ccaccaattt	catttcacgc	gccagggcgg	ctgcagttgg	60
aggccgaggg	cagccctctg	ctcaactaat	gtcttgcatt	tgctgactgc	tgccccgcagt	120
gctgaacatg	ccccacccgc	caggcccagc	actgctgtt	gggtcagcat	ctagtgcgtc	180
tgtcacatct	ttgtctgcac	agccagtagg	attgcctcag	ccagggggtt	tatcagaagg	240
tgtgcaaggg	ctttggggga	actgagcccc	tatagtggc	agtctccctt	accttcccac	300
ctccctgaaa	agcacagaag	acagtgcctt	ggtttgcgtt	ttgaagcaaa	caagtcagct	360
ttctggcttt	gccccaaaac	tgtgatggaa	cataataaaa	ctggagatat	ggtttttaac	420
actgcaaaaaa	ggaaaaaagca	tcaagtttct	acttctggct	ggaaaagcaaa	accaatctca	480
gctgacaagg	ctgggcaaaac	taagtttcc	tgagccatt	ttcctttgag	ccctgaccta	540
ncctgcctta	cctcattaag	gtttggtaa	agcattggaa	aggagganga	ngcangggtg	600
gatgggggg						608

<210> 95

<211> 706

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(706)

<223> n = A,T,C or G

<400> 95

agaataatga	gtacacaagt	ttttgcctat	ccctttcctt	aaaatataag	aaataaaagga	60
gctcttacga	aaaacccagg	ttagaccgca	taaaaaataaa	agtgaacagt	gagggtggtag	120
caagacttct	tttttagaaaa	gaaagcattt	acctgcctgt	ctgttaagggt	aaaatttcat	180
cagtttgcaa	acgataagaa	atgcagactt	gctcttgata	aaaatgttta	aaaacactct	240
ggggggggaa	aaagctcctt	ccatatactg	tgagacattt	gttaagtgcac	atctatttgg	300
tatcagcttt	taaggataaa	aaaggatattt	taaaagttgg	atatttagga	tatgtggagga	360
tattccttta	tgagctctcc	atatccttct	tgagaaaactg	gtttaaaaaaag	aatagggggt	420
tgagtgttac	agagagtagt	ctgaagattc	ctgtgtaaaa	gcaagctaa	caagcaatga	480
agacatgaag	caaataacta	atctaattgt	gtaaagaaaag	gatattttaa	taagttcttt	540
ctgccttgcgt	ctaagagttt	gctaaagtgt	catgaattat	tctggttatt	actaaagttt	600
ctatgaaaca	agtagatttt	aagaataaaat	gtttctggaa	aagaactatg	ttatgatttt	660
gtanaaaatgt	aaagattact	tgaggtgttt	aaaataaaatt	tttcat		706

<210> 96

<211> 719

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(719)

<223> n = A,T,C or G

<400> 96

ccaggccctg	ttccctgcccc	agtggcggct	gctgtgggtt	caggcccagg	ggggccctgna	60
gaagctgtgc	agctgaagag	agggttcaaa	cggaagccga	gaacttgaca	ctgttcaccc	120

caacacccctca cctcccccaag gacatTTGGA agaaaAGCAGC gccaggattc ctcggcagtc	180
gtccccccccc gcacccTgcag tocccctcatg tgctgttctg ctgccccact cagtcctgg	240
accctgtccct ttcatcccgc taaAGCACCC cctaaaaACCC cttcatcaact ttcatTTCTCA	300
gaaaaaaAGTA attgAGCACC TCTCTAGGC GCTGGGGAGT CCACACTGAA CAAAAGAAAC	360
agaaaaaACCT GTCCTCCAGC AGTTGAGTTC TAGGGCAGGG AGACAGAGTT TACAAGATAA	420
gaaaaaATAAT TATGTTAGTAT GCTGCAAGTT AACTGCTGTG TGGAAATCC AGCAGGGGGT	480
GGGATGTGTG ATTGAAATTG AGGGCCACAC TGCCCAAGGTC GTGCTCCGTC AAGGGGGTGA	540
CAGGAGCAAC AGGGGTGGCT GAGTAANGG TTGCAAGCTGG AGGCAACAGC ACATGCAAAG	600
GGCCCTGAGCC AGGATGTGCT GCAATAANGG CCACTGAGGG GGACAGTGTG NGTTGGGGGG	660
TGANGAATGT ATTAAAAAGA NGAAAATTTG CCTTTAAAAA AAAAAAaaaaaA AAAAAAaaaaaA	719

<210> 97
 <211> 572
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(572)
 <223> n = A,T,C or G

<400> 97

gcttggctaa ttTCCAAATT ATTGCATAAT ATGTTCTACC TTAAGAAAAC AGGTTTATGT	60
ACAAAAGTAA TGGTGTGAA TGGATGATGT CAGTTCATGG GCCTTAGCA TAGTTTAAG	120
CATCCTTTTT TTTTTTTTTT TTTTGAAGN GTGTTAGCAT CTTGTTACTC AAAGGATAAG	180
ACAGACAATA ATACTTCACT GAATATTAAAT AATCTTACT AGTTTACCTC CTCTGCTTT	240
TGCCACCCCGA TAACTGGATA TCTTTCCCTT CAAAGGACCC TAAACTGATT GAAATTAAAG	300
ATATGTATCA AAAACATTAT TTCAATTAAAT GCACATCTGT TTTGCTGTT TTGAGCAGTG	360
TGCACTTTAG GGTTCATGAT AAATCATTGA ACCACATGTG TAACAACTGA ATGCCAAATC	420
TAAACTCAT TAAAGAAATA ACAAAATTAGG TTTGACACC CATTCTTAAT TGGAAATAATG	480
GATCAAAAT AGNGGNTCAT GACCTTACCA AACACCCCTG CTACTAATAA AATCAAATAA	540
CCCTTAGAAG GGTATGTATT TTGTTAGGGTGG	572

<210> 98
 <211> 520
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(520)
 <223> n = A,T,C or G

<400> 98

TCAAGCCTGGG GTCCTCCTACT TCTGGAGGCC TCTAGGTCT ATCAGCAACT GGGGGACANA	60
ACAGCAGAGC TGGAGAGTCT GGAGCTGCTA GTTGGAGGCC TGAATGTCCC ATGCAAGTCC	120
AAAGCCCCCGC AGTTTCTCAT TGAGGTAGAA TTACTACTGC CACCACCTGA CCTAGCCTCA	180
CCCTTCATT GTGGCACTCA GAGCCAGACC AAGCACATAC TAGCAAGCAG GGCAGGAGAC	240
GCTGCAGAGC ATTACTGGA CCTGCTGGCC CTGTTGCTGG ATAGCTCGGA GCCAAGGTT	300
TCCCCACCCCT CCTCCCTCTC AGGGCCCTGT ATGCCTGAGG TGTGTTGGG GGCAGCGGTA	360
GCACGTATCC AGGCAGGAGC AGCCCAAGAT GCTTGTACTC TATGTTGAGGA GTTGTCTCANC	420
CGCACATCAT CTCTGCTACC CAAGATGTCC CGGCTGTGGN AAGATGCCAN AAAANGAAC	480
AAANGAACCTGC CATACTGNCC ACTCTGGTC TCTGCCACCC	520

<210> 99

<211> 470
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(470)
 <223> n = A,T,C or G

<400> 99

tttttttcaa	agcaattgt	acacctac	gtggaccaag	aaaaaaaacca	aatcatccnc	60
aatcttcag	ttccacaaca	acaccattat	aaaaacagt	tgatctgaag	tggttccaaa	120
tcttttcttat	cttcaagatc	tatgattagt	aattctgact	cggtcaag	caacatattt	180
ttttagat	tggttgagc	cccgaggagaa	tgtcagagtc	ctgtccactt	ggacatgggt	240
ggagggggagg	ttggcaggg	ctgataaaaag	actagtacgc	ctcgtgtctc	ttcagtctta	300
ttttgc	caaacat	aaggtttttgc	ctactccaag	ttttggtagc	ccaagctcat	360
caaaggatgt	gtctattat	tgntancat	agtaaaaatg	gctctaaatt	gcatataaat	420
ggccagattt	taataatcta	ttgnntcana	agaaaacaac	agnanngngt		470

<210> 100
 <211> 570
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(570)
 <223> n = A,T,C or G

<400> 100

agtttttatt	ttttctgt	acgccccatcc	tgcctgcagt	agaccctttg	ggcttaagan	60
gtcctacaga	ttctaata	agt	ttcccttttgc	tagatgttt	aaatacttag	120
gacatggcc	gttacgtgac	agatgggttt	taacatattt	gtcatatgaa	gaacactctc	180
tgtggggccaa	tggagggtgt	ccttaaaatt	cttcatcttgc	cctgattttgc	tttgcataac	240
ttctggagag	tctgtgtct	cctcatctag	gccaccttgc	cattttttgt	gaaagatgac	300
cttgcctctg	cagtctccgc	caggagtcac	acagctttc	acagcagctg	ccatctttaa	360
ttctttttcc	tgagattcca	gcaagggtgt	gacattgtca	ctttttttgtt	ctagactctt	420
ttaaatttttcc	tgcatttgcc	tggaaagcac	ccctgttaaga	atagatttct	catggctcta	480
aaaatttatttcc	ccaagaatac	cttacttggt	tcaaaagcag	actgtttctc	ttcattttcat	540
ctcaaatac	acttctggc	aagatgttct				570

<210> 101
 <211> 365
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(365)
 <223> n = A,T,C or G

<400> 101

atcaataaaac	caaggtaat	cctnagggtt	ccctcccagt	cctncatca	gctctggcct	60
catcaccaag	gtcacanagn	acacagggga	gggggaanac	ccacncacac	tccttggaaat	120
gggtcctgtt	atttatgttt	ggngcncagn	catattanaa	aaaaaaa	agctttgtat	180

tntttttccn catatnatgg ntgctgtta cacaccctgc caatgcntta gcnnntggaga	240
gtcttttgcata atatgnnggg gaaaggggag ggagggaaatg aaagtgc当地 agaaaaacatg	300
tttttaanaaa ctngggtttt atacaataga atgttttcta gcagaaaaaa aaaaaaaaaa	360
aaaaaa	365
<210> 102	
<211> 546	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(546)	
<223> n = A,T,C or G	
<400> 102	
antgacacac tagccccctg ccgcctcggc atgaacagca tggcaccat ggatggcactg	60
ctgatggtgg taggaagcan aagggtctt gggcagaaag ggcttggtn gaggtgaaac	120
cccnccctca agcctggat ggctgaggc ctggggggccg ggctgccagc tntgggtagt	180
ntgtgggtgg agtganatt tatggtgctt ttccggggcc tgcctatgga ccaatcagca	240
tgcacttctt cccttntgag cccataaaaaa ccctggattc agccagactt ggacanatgt	300
caatactacc aactgtggga agaagctacc cacttcaggaa ctcttgact cctcaggatg	360
acctgcctac anaaagaagc taccctactat gggtnntntn tntgctgana gctggatact	420
ngtcaggatg acctgcctgc anaaaanagct acccnccatg ggttcctnt gaactgtct	480
gttgc当地 aaagctcctn tccttttgc tcnccctcca aaaaaaaaaa aaaaaaaaaa	540
aaaaaa	546
<210> 103	
<211> 376	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(376)	
<223> n = A,T,C or G	
<400> 103	
ctcaactccc ncttcacctt atgtaatgtc tggcctgag atttctctt ggctttantt	60
tcttgatgtt cctgtgatat ggcttctgcc agcaatggaa acaaggctt tatagtagtn	120
ctccatggag tccagttcat cctggggcgt tctccttgc tcatctcgct tttctttggc	180
atagtttctt aggtctcgta atctttgtt ttgaatgttt aaaccttctt caaacagttt	240
cttaaatatc atttcttccc gggctctcat tctcatcatt tttgc当地 actgaactct	300
ataatcatca taatattttc gagcacgaac gatttgctgn cgatnttctt ttatctttga	360
ttgggncaac ctttgc	376
<210> 104	
<211> 700	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(700)	
<223> n = A,T,C or G	

<400> 104
 tttgaaaata cagattttta ccaactttgg attctttttt agttatatgt ttgtctttcc 60
 tttttaattt gttcaaaaact attttttaat ggtcaagtta ctaacacttg aaaatcgat 120
 actgcaccaa atacagtgtt ttccgtagt gtttttaatg agtgcaccta ttactactgt 180
 gcgagaattc atgttttacc agtcattgtt atattacaaa cagacttgca tgattaacca 240
 gttgttacac ttacttttc aagttggagt atatatgact cagtgcagac tggctctct 300
 tatgtgaatg cacacatgca gaaatgcaga gtcaattta catgcccata aagacatttg 360
 taaaagaattc agctctttag gtctgttgta taaatgtgtt tctaggact ttggaatttg 420
 acctcacaga tggtaacaact tgatcagtgc tttgacttaa tttgtggnag ctatctgtat 480
 gttttgaat cttaaatacag acatgcttcc caaaaagatt aatacagaac catcctgccc 540
 ttttggataa gtctatccag ctgtggaaag ggcaacctgt ggtttctctg tactgggtt 600
 taatggggga agaatatgaa cagctttaaa gagctgtgtt ttgggggtac tactattaaa 660
 aaataagatc tgcacgagtc tgactggcct ttgggtggcc 700

<210> 105
<211> 729
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(729)
<223> n = A,T,C or G

<400> 105
 taaaacccctc acactgagaa ctgcttgggtt gggagagagc tgggtgggtt gatctttcc 60
 gagtgtgact tacctccctc aaggggatgt ttaagcttct cgggcagaag tgggtgtct 120
 attcctgaca ccaaacaccc tggtatatgt ggttgcaca ctcagctagt gatgataaaag 180
 gtgttcttaa atatgttagc ttccagtttt cctgaggaaag caattttatg gatactttcc 240
 cctccttctc aagtggggaa tagcagagca aattttatggaaacttaaa ccaatagttt 300
 taaccaataag tttcaacccctc ctgcctcacc actgcttctt tcctgagctc ttccccccaca 360
 cctcaaaaag agtacaaaatg gattccatct gcagaggtaa attctttgtt taaaaaaatgt 420
 ctgtttttct tatctttctt ggttctccta ggtatcagaa caagggtttaa tagaaatcc 480
 taaaaaaatgtt agccaacaaa cagaaaagac aacaacatgtt aaagtaatgtt tccccanatg 540
 cttgtggcaa atgaaaatgtt ggatacttta aagattaatgtt ttgagttatc atctaccaca 600
 catatttttc agcccanaga cattttccctt ttgtcaaaaca cgtggaaatgtt tggggagaaa 660
 ngctgaatctt gttggggag ggttcttaattt ttataggtt ctgtactccca ttccccccctt 720
 ttaattcac 729

<210> 106
<211> 481
<212> DNA
<213> Homo sapien

<400> 106
 gaaaagcaga gtcagctact gagagctctg gaaaagaagga tgcataagaag gtggaaatcc 60
 aaagcctaga aataaaatgtt taaatggaa actgcttattt tcttgcattt atcttcaat 120
 gctaatttgc agttccatgt tattcatgtt actctaaagaa aaatcttctt ggttttgatt 180
 ttctgcattt ttatatattt ttacaatgtt ttcttacccatgaaatgttgc tttatatttt 240
 atggcattctt agtatttttg tgcactgtat tttgtgcatt tcatgtcttc atcaaaaatcc 300
 tctcagtcctt ttttcttttg aagcttgc tgcaggatgtt gctttctat gttttatgt 360
 ccgcgtctttt gaaaagagaac ctatgttca tagttgtattt attgttgcattt catactttaa 420
 attttatatgg ctgtggaaaa acgaattaaa atgttttgag gaaaaaaa aaaaaaaaaaa 480
 a 481

<210> 107
 <211> 519
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(519)
 <223> n = A,T,C or G

<400> 107

cagtcctct cctgcacagag ctaggcaggc gccgaagtag ccgcattggcc ccgtcagant	60
accccccaggaa ctggagagcc aacctcaaag gcaccatccg tgagacaggc ctggagacca	120
gctccgggtgg gaagctggct ggccatcaga agaccgtccc cacggctcac ctgacttttg	180
ttattgactg caccacacggg aagcagctct ccctggcagc aaccgcacatca ccaccccaag	240
ccccccagttcc caatcgaggg cttgtcacc caccatgaa gacctacatc gtgttctgtg	300
ggggaaaactg gccccatctg actcgggtga ccccccattggg tgggggatgc cttgcccagg	360
ccaggggccac cctgcgcctc tgcagagggt ctgtggcctc agcttccttc ccagtcaagcc	420
cgctctgcctt ccaggagggtt cccgaggcta agggaaaacc cgtgaaggct ggcctgtga	480
ggtcttcaac ttgggaaca gtcaaggact cactgaaaag	519

<210> 108

<211> 669
 <212> DNA
 <213> Homo sapien

<400> 108

ggacaatgaa gactgaacta tcgcacatta cctaagaaaag atggaaattt acatgcacat	60
cacaatttgcata tacacaacag aaatttttgcata atcatgagat atacattccg gtgtgtgaca	120
gattggcaca tgacataatc tgggttcttt atagactcag ttgttttggg gcatatctaga	180
ttatcaagag aagggcccttc atgccttagct ttatcttgcata ccaaccacca gggcccttgc	240
ttctgagcag gaagcagctg gggaaatagggc tctttctttt aatgacttcc aacatagttc	300
tctcaaacct tactcttcca gaaggccacc ctcacccatggc tatggctact tcagaaaaaa	360
cttggccctct ggtataatag agcagaatca tcacccatcata ttctatttca agccaaagtc	420
aatatctcaa aggctggttc tgcattttat ttggcttgcata ggagctccta ctgaaagtgc	480
tgaaatgtcg tactgacact tcagactttt agctacccatc actccaaagta agatttatct	540
ctgactggag ggtttcttctt attaaaaacc aaagagtttgcata gggtgccttc acctgtcttgc	600
taatcttcttgcata tgcccttaatg ggaagaatgg gagcagcaga caagtttgcata caggaaggag	660
aacccaaagc	669

<210> 109

<211> 349
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(349)
 <223> n = A,T,C or G

<400> 109

tttcaagccg gattttgggc ctgcttaaac cacttaatg tanttaatgc cagatggttt	60
gaggtttaaa agtcttctgg agaaagcccg ccagagaaca ttcccttgcata agcccccattgt	120
aaaaatacgt gtgggagaga aagtgttttc tctgacttcttgcata aacttc	180

tgaactgtca ggagtattca aaataagact gcctttagg taaggctgtg gtagctttt	240
tgagcacagg ataaaatact tgagtctttg cttaaatgtt actttctcaa tgaggcttg	300
tatgactaaa taaaatctgt ataatccccca aaaaaaaaaa aaaaaaaaaa	349
<210> 110	
<211> 337	
<212> DNA	
<213> Homo sapien	
<400> 110	
ggccttccc actggccat ctggtttct ctccagggtc ttgcaaaatt cctgacgaga	60
taagcagttt tgcaccaactca cgtgcaaaagc caccacacgc cactcagaaa agacgcacca	120
gcccagaagt gcagaactgc agtcaactgca cgtttccatc tctagggacc agaaccaaac	180
ccaccctttc tacttccaag acttattttc acatgtgggg aggttaatct aggaatgact	240
cgtttaaggc ctatttcat gatttttttgc tagcattgg tgcttgacgt attattgtcc	300
tttatttcca aataatatgt ttccctccct caaaaaaaaaa	337
<210> 111	
<211> 552	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(552)	
<223> n = A,T,C or G	
<400> 111	
attttgcatttttca gtttctttaa tggctgaaca gaaagaagct tcaagtaatg gagaaggcat	60
tgtctgatgtt cagctgtttt cctggacgccc tggccgttc ctgtcttcca aatcctatgc	120
ttggaggccc ctggaggtac attttgcctt ggaaccaacc tgaccttaaa aagatgagtg	180
tgacacagcc ggctggcag gaggatggag gtgccacagg acaccacctg cccacgcctt	240
ggccagcctg gccatgtgc cgagtgcggg gaggccaccc caccaggagg gcacagggca	300
aacccttaagc acgggggtat tgcccttgaa gccccagggg atgcccgttg cggatcctc	360
atgccttattt gactagctg ctggctgaag gagccagggg gcctgagcct gcaacactgc	420
aagggggttag aagggtatgc tgctgtggc gccactggac tcaaacctca cattanaagc	480
tacaaaagaac cccaaatgcg ctcaanagc cccaccaacc cccaaagccan gtcatnccct	540
gacacantga at	552
<210> 112	
<211> 115	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(115)	
<223> n = A,T,C or G	
<400> 112	
gtcccttagtta canaaacttc ccaaacaana actatgcncg ancncatccc cttegagtc	60
tctncnttct gctccgttc ccatggnttg ccccatatca taaggtacgc tggga	115
<210> 113	
<211> 649	

<212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(649)
 <223> n = A,T,C or G

<400> 113

gcctgattaa	aaactaaagca	gaagtagttt	taacanaaaat	actcatgaaa	atgtttngaa	60
actgaaattt	aaacaactgt	aatattaagg	aaaccagaat	caataaatca	ctgtcttgcc	120
agcacagcta	cagagtaaca	tgattcaggg	gaggaagtt	ccttagagtt	acttttataa	180
ttcttttttt	tttccttta	ggtttanaaa	tcttacaaaat	ttaaacttta	tcctttttaaa	240
attatgttga	cataatttag	atattgttaag	cttaaaataac	aaatgtttat	agataacctc	300
tttaccataa	actaatccct	ggcaagccat	ggctctttt	tttttttgggt	gtttaaagcc	360
tgtaaacagt	ttttctgaat	gatcatgaac	tttcttggg	tttagcacta	ggattttagct	420
atgaagagag	ctcataggct	ttcaggtgct	aattgagatc	tgccctgtta	gagtcttggg	480
gtgcttagatt	ggtcacattt	acaccagtgg	cagggaaaggc	atctatgagt	ttgatgttt	540
ttatcacaca	cttcagntgt	tttagaaagtt	attaccaata	cttttaaaca	acactccaaag	600
aaaatttgct	atatttcttt	ctcatcacta	cagagagagt	agatttccc		649

<210> 114

<211> 650
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(650)
 <223> n = A,T,C or G

<400> 114

tggcgattgg	tgttggcggt	ctggctcagc	tgggcagggg	gtaactttac	tgatttgggg	60
gtggttttta	gtttaatttt	tcttttctag	cttcccatcg	acggtcagtg	cgcacgttgt	120
aatcagctga	ggccatgtca	ggagacggag	ccacggagca	ggcagctgag	tatgtcccg	180
agaagggtgaa	gaaagcggaa	aagaaaattag	aagagaatcc	atatgacctt	gatgcttgg	240
gcatttcrcat	tcgagaggca	caggttttagt	gatataaggat	tacatttct	tctctatggg	300
tccaaatcaca	ctacttggtt	ctgcagtgaa	taatatttca	ataatctaa	cattgttaat	360
gtctgtttatt	ggttttcaat	tttagaatca	acctataagac	aaagcacgga	agacttatga	420
acgccttggt	gcccagttcc	ccagttctgg	cagattctgg	aaactgtaca	ttgaagcaga	480
ggttactatt	ttattttatt	tttcttata	tcagttttg	cagcattcac	tgttagtata	540
aaaaacaaag	ttangaaacat	agccaattan	gacaaggagg	attaaatgt	gtcttacett	600
tattttgtaa	aataggata	aaggagtaat	taaaatgaat	ttttgaaatt		650

<210> 115

<211> 403
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(403)
 <223> n = A,T,C or G

<400> 115

gtattatgac tttaaaaacc ccattattga aaagtacctg acaaggcagc tcacgaancc	60
caggcctgtg atcctggacc cgccggaccc tachnngaaac ttgggtggng gagacccaan	120
gggnnggagg canctggcac angaggctga ggcctgnctg aattacccat gctttaagaa	180
tngggatggg necccantga gctcctgnat tctgctggtg anacctcctg ctteccctc	240
gccattcatic cctgccccctc tccatgaagc ttganacata tanctggaga ccattcttc	300
caaanaactt acctnttgcc aaaggccatt tatattcata tagtgacang ctgtgctcca	360
tattttacag tcattttgggn cacaatcgag ggtnctgga att	403
<210> 116	
<211> 397	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1) ... (397)	
<223> n = A,T,C or G	
<400> 116	
cgaaagaaaa aaagtatgat tggaccctgg aaagattttgg aaacttgagt ggtttgataa	60
cccttctatg tattgttaggg agaaaaaaaaa aagtttattt tattccactg tcctccotta	120
aaagcatcat ttganzaata aatgaatattt gtctttaaac caagggttag ggaattttcc	180
tctctctctc tctctccctc ctctttctgt tcaaaagaact tcaaacattt gggaccacct	240
ggtattctgt attttcaactg gccatattgg aagcaggcttct agttgcattt gattgagttg	300
tgctggcagt agtttccatg cctgtcaatg tattcatagtc ctttgttgc cagataaata	360
aatatttgat acgctttaaa aaaaaaaaaa aaaaaaaaaa	397
<210> 117	
<211> 59	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1) ... (59)	
<223> n = A,T,C or G	
<400> 117	
cacttatggg gacaatggga agactcttct tttncactgg actgtacctg gacntnnnaa	59
<210> 118	
<211> 751	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1) ... (751)	
<223> n = A,T,C or G	
<400> 118	
catcaacata cccgctttat tgctgactca tgacaactaa tgggaagaca tggctcagat	60
gtgcagccac agtgagcttc tgaacatttc ttctcagact aagctttag acacagtgc	120
agttgaaaga aagaattgct tgacatggcc acaggagcag gcagcttcct gcagacatga	180
cagtcaacgc aaactcatgt cactgtgggc agacacatgt ttgcaaagag actcagagcc	240

aaacaaggcac actcaatgtg ctttgcggaa atttacccat taggtaaatc ttccctcetc	300
ccaagaagaa agtggagaga gcatgagtcc tcacatggaa acttgaagtc agggaaatga	360
aggctcacca attatttgtg catgggtta agttttcctt gaaattaagt tcaggttgt	420
ctttgtgtgt accaattaat gacaagaggt tagatagaag tatgttagat ggcaaagaga	480
aatatgtttt gtgtcttcaa ttttgcataa aataaccag aacatggata attcatttat	540
taattgtatt tggtaagcca agtcttattt ggagaaaaatt aatagttttt ctaaaaaaga	600
attttctcaa tatcacctgg ctgtataaca tttttctct tcgagttct ttttctggag	660
tttaacaaac ttgttcttta caaatagatt atattgacta cctctcaactg atgnatgat	720
attaagttctt attgttactt ttggatttct a	751

<210> 119

<211> 591

<212> DNA

<213> Homo sapien

<400> 119

aggcttcttg tcacactgaa cacatccgc cacaggcacc agctgggtgg gaccagcagc	60
ccccagcata ctcttgcact ggctggcaca aaaagaaaacc tgctgtatac cccccaagt	120
gtccctttcc caattaccc tggggctctc tgctgcttgc ctctgctgt ctggactggg	180
agagcttctg tcctgtctg catgggtatt tagactgtgg gggagatgcc ctttcttata	240
gcactggagg aggaaaacaa attcttgcctt ccctcagaat gagagtggct ttttctgtt	300
tgcaaggggca ctatggtcag ggcaaaaggca tggcccagggt gtttaagtac agggtgacgt	360
gtgcctatgc aatggggtgg taaggcaggc acgaagagtc caaaaaatct aggtggctc	420
tcaagctctgc cacctcttagc tgcatgaccc tggcaagct atgtaaaaacc aattgcctgc	480
tccattaaag actgtgaagg tagaatgttt gtaaagctct taacagtatg taaggcttca	540
ataaaatttca gttttccctt tggatttctt atcaaaaaaaaaaaaaaaa a	591

<210> 120

<211> 652

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(652)

<223> n = A,T,C or G

<400> 120

attttgcagt acattaaaac tgaggcccag agatgtgatt tgcttgaggc cacacagcta	60
gatttttgggt ggaagtgggc ctggaaacaca gtgtactttc tgctgtttct gactgtaaaa	120
cccaagttctc gtcctctgag ttccatcttcc aagccccctt ccattttggc cctatgtgg	180
ctccaccata ttccacacacc accgcccacca ttggccaatg cctctcttta agcaatatac	240
ccatttcgttc tcttatttggg aactggatgg atgaagcccc aaatttcagcc ccacccacag	300
agaaggccctc ctacactcag cctctgtccaa cccttggcaa atctttcaag ctctctctc	360
caggaaaagtg gggcccccaac tcagtcactc cacccttcc caggtccctg aggtgtggtc	420
tactgtatcc ccatttttttttcc cacaacttcca ctcaccctt acggctccat ccacccat	480
agtttggaaagg cttgtgtttt cagagaggag caatgtgtt cagcgtgtcc cagactccag	540
tgtttacaga tcaccacat ttacaacccaa tccaaatggcc agaagctcc tctaaccana	600
aggagttctg aaggggcaga tgggggtgtg agtagtcggg gagtcgggat tg	652

<210> 121

<211> 407

<212> DNA

<213> Homo sapien

<400> 121
 ctcttttagta tgacactggc aactgaeggc actgcggata tggggat aaggttcaaa 60
 agaagaggct gttctaagaa agactaccga gtaatcaatc acctcctcag agaaagtctg 120
 ctcaggaaac tcttctccca ccagccccctg cacttgggtc cttgcgttgc ctctggctgg 180
 aagctgttgc ccccaacttc agaaaagtgtc tgcatggatcc acaggtctc tcttgggtca 240
 agggaccaggc tctgtgaaca cggcaagtaa caacagagag aaaacgtgag gagaagagag 300
 agaccggat tttgaatcc tggatccatctc accaggcaca cgaaagaata 360
 aaattaagga atcaagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 407

<210> 122
 <211> 752
 <212> DNA
 <213> Homo sapien

<400> 122
 caaatccctc cttatccaggc ttttctgtct ctaataccccc aagcggttacc cctgtcttc 60
 cctcatttccc ggggctgcag gcgcctctca cagtcgcagc tggatccatca ctacatgtgg 120
 ctgccacagc cccatccccca gctccagtc tccctggatt cgccctcagca ttcagttcca 180
 atttcaactc cgctcttgcgc tgcacaagccg gtttattatc tggacttcaa gctgcaggca 240
 gtttctgtttt tccaggccctt ttgtccctcc cgggtatccc tgggtttctt cagaatccctt 300
 cacaatcatc ttgcagaa ttacagcata atgcggctgc acagtcagca ttgttacagc 360
 agtccatcc agtttcggct ctggaaagct atccagctca gctgtatggg tttcttagtt 420
 atcccttcagc gcccggaaaca ccattttctt tgcaaccaag cctgtccctt agtgggtggc 480
 agtgaataact tttaactttt atttcttc agagcaacat cagaatttgc tgagaacttgc 540
 aatgaacaat ctgacaaatg tgaagctggc caaaagtcgg aaaaatgagaa tgagggtaat 600
 cctggagaaa ttgtgacaac aatttggaaa ttgtgggtgc attttaaagt gtgaacactc 660
 ccctatgtaa atatgtcgtc aataaattgg atggagaatg gtatttaaaa agtgtttgg 720
 gactttcac ctgtccata aaaaatttggaa tt 752

<210> 123
 <211> 401
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(401)
 <223> n = A,T,C or G

<400> 123
 atgaacccaaa tagaaataag catcaacat gaacagctgg aagagagttt tcaggaacta 60
 gtggaaaggatt accggcggtt tatttgcacca cttgtctcaag agttaaaggatt atactgtct 120
 gtacaggaag cttgcacccatt ttctgttacaa tggatccatca aaaatctgtat gacttttatt 180
 tttaaaatctt gtgacatccc gcttataacta aaagttatctt atcttttagtt gaatattttc 240
 ttttggagag attgtatatt tttaaaatactt gtttagagtt tatgagcata tattgcattt 300
 aaagaaaatggat aaagcttctg aaataactact gcaatttgctt cccttctttaa acagtataat 360
 aatgtcttag ttgtgatnaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 401

<210> 124
 <211> 103
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1)...(103)

<223> n = A,T,C or G

<400> 124

aagataactt	gctgggacca	catgcctgat	tgccacagct	gtcatcacgt	tatttaatga	60
acctagtgt	gaagacagt	aaaagggtcc	attgacnngt	gcn		103

<210> 125

<211> 1024

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1024)

<223> n = A,T,C or G

<400> 125

gagggcagt	aggagcgagg	agcgggcaga	ggcagctccg	gcggccgaga	ggagggagcg	60
cggcgcagag	aggagggct	tgcgccccgt	agaaatgtca	atcagagcct	ggacccctgc	120
gctcccgcac	cagccccgc	ctcgcgcctg	cagaagccca	agatctggtc	cctcgccgag	180
actgccacaa	gccggacaa	cccgccgcgc	tcgcctcccg	gcccgggggg	gtctccaccc	240
ggggcagcgg	tcgcgccttc	cgcgcgtcag	ctcttcgcgg	ccggccgcgc	cgcggccgct	300
cacagactgg	tctcagegc	gctgggcaag	ttcccggtt	ggaccaaccg	gcgcgtttcca	360
ggcccacccg	ccggcccccg	ccgcaccccg	ctctccctgc	tggctctgc	ccctccgcac	420
ctgctggac	tteccggagc	cgcggccac	ccggctgccc	ccggccgcctt	cgcggccca	480
gcccggcccg	aaggcggAAC	agatcgctgt	agtgcctgg	aagtggagaa	aaagttactc	540
aagacagctt	tccagccctg	gcccaggcgg	ccccagaacc	atctggacgc	cgcctggtc	600
ttatcggtc	tctccatc	ctagttcttt	aaaaaaaaaca	aaaaaaaaacaa	aaaaactttt	660
ttaatcggt	gtataattg	tataaaaaaa	atcgctctgt	atagttacaa	tttgtaagca	720
tgtccgtgt	taaataccta	aaagcaaaac	taaacaaga	aagtaagaaa	aagaaataaaa	780
accagtcc	ctcagccctc	cccaagtcgc	ttctgtggca	ccccgcattc	gctgtgaggt	840
ttgtttgtcc	ggttgatttt	gggggggtgga	gtttcagtg	gaataaacgt	gtctgccttt	900
gtgtgtgtgt	atataatacag	agaaatgtac	atatgtgt	accaaattgt	acgagaaaagt	960
atctatTTT	ggctaaataaa	atgagctgcc	tgccactttg	nctataaaaa	aaaaaaaaaaa	1020
aaaaa						1024

<210> 126

<211> 214

<212> PRT

<213> Homo sapien

<400> 126

Arg	Pro	Arg	Ile	Arg	His	Glu	Glu	Gly	Ser	Glu	Glu	Arg	Gly	Ala	Gly	
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Arg	Gly	Ser	Ser	Gly	Gly	Arg	Glu	Glu	Gly	Ala	Arg	Arg	Arg	Glu	Glu	
						20			25			30				
Gly	Leu	Ala	Pro	Arg	Arg	Asn	Val	Asn	Gln	Ser	Leu	Asp	Pro	Cys	Ala	
						35			40			45				
Pro	Ala	Pro	Ala	Pro	Ala	Ser	Ala	Leu	Gln	Lys	Pro	Lys	Ile	Trp	Ser	
						50			55			60				
Leu	Ala	Glu	Thr	Ala	Thr	Ser	Pro	Asp	Asn	Pro	Arg	Arg	Ser	Pro	Pro	
						65			70			75			80	
Gly	Ala	Gly	Gly	Ser	Pro	Pro	Gly	Ala	Ala	Val	Ala	Pro	Ser	Ala	Leu	
							85			90			95			

Gln Leu Ser Pro Ala Ala Ala Ala Ala Ala His Arg Leu Val Ser
 100 105 110
 Ala Pro Leu Gly Lys Phe Pro Ala Trp Thr Asn Arg Pro Phe Pro Gly
 115 120 125
 Pro Pro Pro Gly Pro Arg Pro His Pro Leu Ser Leu Leu Gly Ser Ala
 130 135 140
 Pro Pro His Leu Leu Gly Leu Pro Gly Ala Ala Gly His Pro Ala Ala
 145 150 155 160
 Ala Ala Ala Phe Ala Arg Pro Ala Glu Pro Glu Gly Gly Thr Asp Arg
 165 170 175
 Cys Ser Ala Leu Glu Val Glu Lys Lys Leu Leu Lys Thr Ala Phe Gln
 180 185 190
 Pro Val Pro Arg Arg Pro Gln Asn His Leu Asp Ala Ala Leu Val Leu
 195 200 205
 Ser Ala Leu Ser Ser Ser
 210

<210> 127
 <211> 507
 <212> PRT
 <213> Homo sapien

<400> 127
 Met Ser Phe Pro Gln Leu Gly Tyr Gln Tyr Ile Arg Pro Leu Tyr Pro
 1 5 10 15
 Pro Glu Arg Pro Gly Ala Ala Gly Gly Gly Gly Ser Ser Ala
 20 25 30
 Gly Gly Arg Ser Gly Pro Gly Ala Gly Ala Ser Glu Leu Ala Ala Ser
 35 40 45
 Gly Ser Leu Ser Asn Val Leu Ser Ser Val Tyr Gly Ala Pro Tyr Ala
 50 55 60
 Ala Ala Ala Ala Ala Ala Ala Gln Gly Tyr Gly Ala Phe Leu
 65 70 75 80
 Pro Tyr Ala Thr Glu Leu Pro Ile Phe Pro Gln Leu Gly Ala Gln Tyr
 85 90 95
 Glu Leu Lys Asp Ser Pro Gly Val Gln His Pro Ala Thr Ala Ala Ala
 100 105 110
 Phe Pro His Pro His Pro Ala Phe Tyr Pro Tyr Gly Gln Tyr Gln Phe
 115 120 125
 Gly Asp Pro Ser Arg Pro Lys Asn Ala Thr Arg Glu Ser Thr Ser Thr
 130 135 140
 Leu Lys Ala Trp Leu Asn Glu His Arg Lys Asn Pro Tyr Pro Thr Lys
 145 150 155 160
 Gly Glu Lys Ile Met Leu Ala Ile Ile Thr Lys Met Thr Leu Thr Gln
 165 170 175
 Val Ser Thr Trp Phe Ala Asn Ala Arg Arg Arg Leu Lys Lys Glu Asn
 180 185 190
 Lys Met Thr Trp Ala Pro Arg Ser Arg Thr Asp Glu Glu Gly Asn Ala
 195 200 205
 Tyr Gly Ser Glu Arg Glu Glu Asp Glu Glu Asp Glu Glu Glu
 210 215 220
 Ser Lys Arg Glu Leu Glu Met Glu Glu Glu Leu Ala Gly Arg Gly
 225 230 235 240
 Gly Gly His Gly Gly Arg Gly Ala Gly Arg Arg Arg Asp Glu Glu

245	250	255
Ile Asp Leu Glu Asn Leu Asp Ser Ala Ala Ala Gly Ser Glu Leu Thr		
260	265	270
Leu Ala Gly Ala Ala His Arg Asn Gly Asp Phe Gly Leu Gly Pro Ile		
275	280	285
Ser Asp Cys Lys Thr Ser Asp Ser Asp Asp Ser Ser Glu Gly Leu Glu		
290	295	300
Asp Arg Pro Leu Ser Val Leu Ser Leu Ala Pro Pro Pro Pro Pro Val		
305	310	315
Ala Arg Ala Pro Ala Ser Pro Pro Ser Pro Pro Ser Ser Leu Asp Pro		320
325	330	335
Cys Ala Pro Ala Pro Ala Pro Ser Ser Ala Leu Gln Lys Pro Lys Ile		
340	345	350
Trp Ser Leu Ala Glu Thr Ala Thr Ser Pro Asp Asn Pro Arg Arg Ser		
355	360	365
Pro Pro Gly Ala Gly Ser Pro Pro Gly Ala Ala Val Ala Pro Pro		
370	375	380
Thr Leu Gln Leu Ser Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala His		
385	390	395
Arg Leu Val Ser Ala Pro Leu Gly Lys Phe Pro Ala Trp Thr Asn Arg		400
405	410	415
Pro Phe Pro Gly Pro Pro Ala Gly Pro Arg Pro His Pro Leu Ser Met		
420	425	430
Leu Gly Ser Ala Pro Gln His Leu Leu Gly Leu Pro Gly Ala Ala Gly		
435	440	445
His Pro Ala Ala Ala Ala Ala Tyr Ala Arg Pro Ala Glu Pro Glu		
450	455	460
Ser Gly Thr Asp Arg Cys Ser Ala Leu Glu Val Glu Lys Lys Leu Leu		
465	470	475
Lys Thr Ala Glu Gln Pro Val Pro Arg Arg Pro Gln Met Arg Leu Asp		480
485	490	495
Ala Ala Leu Val Leu Ser Ala Leu Ser Ser Ser		
500	505	